GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model - protein search, using OM protein October 26, 2004, 06:09:56; Search time 85.5 Seconds (without alignments) 83.913 Million cell updates/sec Run on:

US-10-066-965A-1 129 Title: Perfect

1 QVWSLWALGWRWLRRYGWNM 20 score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 Total number of hits satisfying chosen parameters: Searched:

2002273 segs, 358729299 residues

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_23Sep04:* .: geneseqp1980s:* : geneseqp1990s:* geneseqp2003as:*
geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aar89346 Cdk2-inte	Н	0	Aao18008 Intracell	7	Abg24883 Novel hum	σ	0	Abp70925 Arabidops	4	Aau17861 Novel hum	Adg41241 Human res	Adg22291 Cyanophag		Abg18132 Novel hum			Abo74240 Pseudomon		Adm72293 Equine TL		Abm41765 Propionib	Abo58643 Human gen	Abb90371 Human pol	Abp59544 Human his
SUPPRINTES	ID	AAR89346	AAW32121	AAY49340	AA018008	AA018007	ABG24883	ADG22339	ABP70920	ABP70925	ABP70924	AAU17861	ADG41241	ADG22291	AB076305	ABG18132	AAU36364	ABU38632	ABO74240	AB083419	ADM72293	AAU45246	ABM41765	AB058643	ABB90371	ABP59544
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ð	Query Match	100.0	100.0	100.0	90.7	75.6	50.4	46.9	46.5	46.5	46.5	45.7	45.7	43.4	43.4	42.6	41.1	41.1	41.1	41.1	40.7	40.3	40.3	40.3	40.3	40.3
	Score	129	129	129	117	97.5	65	60.5	09	09	9	53	59	26	56	55	53	53	53	53	52.5	52	52	52	52	52
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	Aau57671 Propionib	Abm54190 Propionib	Aam80357 Human hae	Human	Abg06199 Novel hum	Abg11452 Novel hum	Abu22728 Protein e	Abo82724 Pseudomon	Abr56763 Human sec	Abu21414 Protein e	Abo82339 Pseudomon	Adp98943 C. albica	Abu21411 Protein e	Aam87561 Human imm	Adc78292 Human mig	Ada34903 Acinetoba			Abb93906 Herbicida
AAB48460	AAU57671	ABM54190	AAM80357	ABP01028	ABG06199	ABG11452	ABU22728	AB082724	ABR56763	ABU21414	AB082339	ADP98943	ABU21411	AAM87561	ADC78292	ADA34903	AAB11535	AAG44312	ABB93906
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1725	9	09	68	78	89	105	261	480	136	300	396	513	538	36	41	266	743	391	391
40.3	39.5	39.5	39.5	39.5	39.5		39.5	39.5		39.1	39.1	39.1	39.1	38.8	38.8	38.8	38.8	38.4	38.4
52	51	51	51	51		51	51	51	50.5	50.5	50.5	50.5	50.5	50	50	0.50	50	49.5	49.5
26	27	8 2	6	3.0	31	1 C	8	34	35	98	37	38	68	40	41	42	43	44	45

ALIGNMENTS

AAR89346 standard; peptide; 20 RESULT 1 AAR89346

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AAR89346;

(first entry) 10-SEP-1996 Cdk2-interacting peptide isolated using interaction trap assay.

Cdk2; cyclin dependent kinase 2; assay; identifying; isolating; cell cycle; interaction; antagonist; conformationally-constrained; agonist; interaction trap; thioredoxin; LexA; two-hybrid system.

Synthetic.

WO9602561-A1.

01-FEB-1996.

95WO-US009307. 20-JUL-1995; 94US-00278082. 20-JUL-1994;

(GEHO) GEN HOSPITAL CORP. (GEMY) GENETICS INST INC.

Xu C; Jessen TH, Mccoy JM, Brent R,

WPI; 1996-105852/11.

Interaction trap systems using conformationally-constrained proteins - useful for detection of protein interactions and for identification and isolation of interacting proteins.

Claim 66; Page 60; 73pp; English.

interaction trap assay using conformationally-constrained by an interaction trap assay using conformationally-constrained proteins. The assay comprises providing a host cell (esp. a yeast cell) which contains: (i) a reporter gene operably linked to a DNA-binding protein recognition site, pref. LexA, (ii) a 1st fusion gene expressing Cdk-2 covalently bonded to a LexA binding protein, and (iii) a 2nd fusion gene expressing a conformationally-constrained (pref. with thioredoxin) protein (either expected to interact with Cdk-2 or a random peptide) covalently bonded to a gene-activating moiety, and measuring expression of the reporter gene as a measure of interaction between Cdk2 and the conformationally constrained protein. The same system may be applied to find proteins that

Indels

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Mismatches

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20; Conservative
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ID AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aptamers AAW32116-W32132 have been isolated from a peptide library and are used in a novel interaction trap method for detecting protein the interactions and isolating novel proteins. The method involves a host cell containing a reporter gene operably linked to a DNA-binding-protein (DBP) recognition site, a fusion gene capable of expressing a fusion gene capable of expressing a fusion protein which is able to specifically bind to the DBP recognition site of and a second fusion gene which expresses a second fusion protein which is conformationally constrained and bonded to a gene activating moiety.

Measuring expression of the reporter gene gives a measure of the conformation between Pl and P2. This method can be used to identify agonists or antagonists for use as therapeutic molecules or for the design of simple molecule mimetics. The method is specifically used to detect an interacting protein in a population of proteins or to identify a candidate interactor. Using conformationally constrained proteins conformationally constrained proteins can provide for tertiary structural analysis and can also proteins conformation of the candidate interactor to increase the protein's solubility, incorrect provide to increase the protein's conformation in the capacity of the candidate interactor to
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interact with any other protein of interest (e.g. Ras) or proteins having agonist or antagonist activity on such interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New trap system for detecting protein interactions - comprises a reporter gene linked to a DNA-binding-protein recognition site and fusion proteins to test for interactions.
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                               Protein interaction; interaction trap; fusion protein; mimetic;
                                                                                            0;
                                                                   Length 20;
                                                                                           Indels
                                                               Score 129; DB 2;
Pred. No. 7.1e-10;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                            therapeutic; detection; reporter gene.
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                                                                                                                  1 QVWSLWALGWRWLRRYGWNM 20
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                                                                                                                                                                                                          AAW32121 standard; peptide; 20
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                                                                 100.08;
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                                                                                                                                                                                                                                                           (first entry)
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                                                                                         Conservative
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                                                                            Local Similarity
                                      Sequence 20 AA;
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                                                                                                                                                                                                                                                                                      Interaction
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                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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Length 20;

Score 129; DB 2; Pred. No. 7.1e-10;

100.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             f Saccharomyces and/or mammalian cells comprising recombinant fusion proteins, useful for detecting protein interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to a population of Saccharomyces and/or mammalian
Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces, mammalian, fusion protein, interactor peptide, conformation-constraining protein, DNA binding moiety, Cdk2, gene activating moiety, protein interaction, gene purification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 3B; 24pp; English.
                                                                                                                                                                                           AAY49340 standard; peptide; 20 AA
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                                                                                                                                                                                                                                                                                                                            Cdk2 interacting peptide i5-4.
                                                                     QVWSLWALGWRWLRRYGWNM
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                                                                                                                                                                                                                                                                                   (first entry)
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GENETICS INST INC.
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Les 20; Conservative
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CNRS ) CENT NAT RECH SCI
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N-PSDB; AAS89070.
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                                                                                                                                                                                                            WPI; 2002-418829/45.
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Best Local Similarity
                                                                                                                                                                            Brent R,
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15-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a process for specifically modulating the properties of an intracellular target molecule T, and/or of a cellular component C which interacts directly or indirectly in a cell with the target. The process involves the introduction into the cell of chimeric molecule known as a targeted effector, comprising a recognition moiety capable of recognising T and an effector moiety. The chimeric protein or nucleic acid can be used in the preparation of a medicament for the treatment of microbial infections, immunological disorders, myopathies, genetic disorders, metabolic disorders, psychiatric disorders, myopathies, genetic disorders, cardiovascular disorders and dental disorders. The present sequence is a mutant of a known anti-Cdk2 aptamer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intracellular target; cellular component; property modulation; antimicrobial; immunomodulatory; nootropic; neuroprotective; metabolic; neuroleptic; cytostatic; cardiant; infection; immunological disorder; neurological disorder; metabolic disorder; psychiatric disorder; myopathy; cancer; cardiovascular disorder.
Intracellular target; cellular component; property modulation; antimicrobial; immunomodulatory; nootropic; neuroprotective; metabolic; neuroleptic; cytostatic; cardiant; infection; immunological disorder; neurological disorder; metabolic disorder; psychiatric disorder; myopathy; cancer; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                           Process for specifically modulating the properties of an intracellular target molecule used for the treatment of various disorders.
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                                                                                                                                                                                                                                                                                                                                                           Cohen BA;
                                                                                                                                                                                                                  13-NOV-2000; 2000EP-00403156.
                                                                                                                                                                                                                                                     13-NOV-2000; 2000EP-00403156.
                                                                                                                                                                                                                                                                                                        (MASS-) MASSACHUSETTS GEN H
(MOLE-) MOLECULAR SCI INST.
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 AA;
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The present invention relates to a process for specifically modulating the properties of an intracellular target molecule T, and/or of a cellular component C which interacts directly or indirectly in a cell with the target. The process involves the introduction into the cell of chimeric molecule known as a targeted effector, comprising a recognition moiety capable of recognising T and an effector moiety. The chimeric protein or nucleic acid can be used in the preparation of a medicament for the treatment of microbial infections, immunological disorders, neurological disorders, metabolic disorders, psychiatric disorders, neurological disorders, cardiovascular disorders and dental disorders. The present sequence is a known anti-Cdk2 aptamer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            Process for specifically modulating the properties of an intracellular target molecule used for the treatment of various disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.6%; Score 97.5; DB 5; Length 17; 80.0%; Pred. No. 6.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #24874.
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                                                                                                                                                                             GEN HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVWSLWALGWRWLRRYGWNM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OVWSLWALGWRW---YGWKM 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US008631.
13-NOV-2000; 2000EP-00403156.
                                                                          13-NOV-2000; 2000EP-00403156.
                                                                                                                                                                                                                                                                                                      Cohen BA
                                                                                                                                                                                (MASS-) MASSACHUSETTS GEN H(MOLE-) MOLECULAR SCI INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging convolvesphide and polynucleotide sequences have applications in the purposable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the vivial patences.
               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galisson F, Bouzon M, Robert C, Vico V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CNRS ) CNRS CENT NAT RECH SCI.
(GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 4;
Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                            Claim 20; SEQ ID NO 55242; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyanophage S-2L encoded protein #84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-2002; 2002FR-00005424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-2002; 2002FR-00005424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG22339 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 WSLWALGWRWLRRYG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 WALWSRGWRLLRRLG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marliere P, Kaminski PA,
Weissenbach J, Saurin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaminski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyanophage S-2L.
                                                                        biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2839079-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG22339;
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Length 118; 3; Indels

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Pochet S;

WPI; 2004-045746/05. N-PSDB; ADG22255.

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The invention relates to the entire genome of cyanophage S-2L, and to the protein encoded by it. Genes isolated from the genome of S-2L are useful for preparing enzymes for synthesis of D-bases (D = 2,6-diaminopurine), particularly D, dDMP and dDTP, or polymucleotides containing these bases, polymerases involved in metabolism of D-bases and decoxpucleotide analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides, on be used for detection and/or identification of S-2L, and for identifying agents that modulare synthesis of D-bases or polymucleotides containing them, and fusions of S-2L polypeptides with an antigen can be used to raise specific anibodies, useful for detecting S-2L. This sequence corresponds to one of the proteins encoded by the cyanophage S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Altering seed characteristics for producing transgenic plants by introducing into a plant cell a recombinant expression cassette having a polynucleotide that alters the number, type and configuration of aleurone
genomic sequence for cyanophage S-2L, useful for identifying genes synthesis of 2,6-diaminopurine bases or polynucleotides containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for altering seed characteristics. The method comprises introducing (into a plant cell) recombinant expression cassette comprising a polymucleotide whose expression, alone and in combination with additional polymucleotides,
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gruis DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; seed; grain; aleurone cell; transgenic plant; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                  Score 60.5; DB 8; Length 78; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jung R,
                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ນີ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SE, Li C,
Wang CW;
                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen B, Lid
Lorentzen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 75-80; 171pp; English.
                                                            Claim 6; SEQ ID NO 85; 423pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP70920 standard; protein; 2115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                 46.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2001; 2001US-0309719P. 25-OCT-2001; 2001US-0337444P.
                                                                                                                                                                                                                                                                                                                                                                                                               3 WSLWALGWRWLRRYG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                       |:||: ||||| :|
44 WALWS~AWRWLRSWG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olsen O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tarczynski MC, Olsen O,
Ananiev E, Nichols SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-248094/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis calpain.
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells within seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACC42644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003011015-A2.
                                                                                                                                                                                                                                                                                                                 Sequence 78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2003.
                                                                                                                                                                                                                                                                                    2L genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP70920;
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calpain.
                                them.
                                                                                                                                                                                                                                                                                                                                                                                Matches
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Gaps

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Indels

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Mismatches

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Conservative

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Matches

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The present invention relates to a method for altering seed characteristics. The method comprises introducing (into a plant cell) a recombinant expression cassette comprising a polynucleotide whose expression, alone and in combination with additional polynucleotide is alters the number, type and configuration of aleurone cells within seed, (the polynucleotide is operably linked to a promoter). The method is useful for altering seed characteristics to produce a transgenic having seeds and grains with improved nutritional, industrial and agricultural traits. The present sequence is Arabidopsis thaliana DEK1, which was used to illustrate the invention. The Dek1 protein is involved in aleurone
                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Altering seed characteristics for producing transgenic plants by introducing into a plant cell a recombinant expression cassette having a polynucleotide that alters the number, type and configuration of aleurone cells within seed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; seed; grain; aleurone cell; transgenic plant; gene therapy; dekl; aleurone cell differentiation.
alters the number, type and configuration of aleurone cells within seed, (the polynucleotide is operably linked to a promoter). The method is useful for altering seed characteristics to produce a transgenic having seeds and grains with improved nutritional, industrial and agricultural traits. The present sequence is the protein sequence for calpain, which was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruis DB;
                                                                                                                                                                                           Gaps
                                                                                                                                                                                           0
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Lorentzen JA, Wang CW;
                                                                                                                                                        46.5%; Score 60; DB 6; Length 2115; 56.2%; Pred. No. 51;
                                                                                                                                                                                           Indels
                                                                                                                                                                                           . 9
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 149-154; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                  ABP70925 standard; protein; 2150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2001; 2001US-0309719P.
25-OCT-2001; 2001US-0337444P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-2002, 2002WO-US024438
                                                                                                                                                                                                                             3 WSLWALGWRWLRRYGW 18
                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                              WILWAVNWRPWRLYSW
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olsen O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rarczynski MC, Olsen O,
Ananiev E, Nichols SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                           Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-248094/24.
                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                           Sequence 2115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACC42661
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                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                   ABP70925;
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                                                                                                                                                                                                                                                                                                                  RESULT
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Length 2150;

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Score 60; Pred. No.

46.5%; 56.2%;

Query Match Best Local Similarity

AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altering seed characteristics for producing transgenic plants by introducing into a plant cell a recombinant expression cassette having a polynucleotide that alters the number, type and configuration of aleurone
                                                                                                                                                                                                              Plant; maize; seed; grain; aleurone cell; transgenic plant; gene therapy; dekl; aleurone cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for altering seed characteristics. The method comprises introducing (into a plant cell) a recombinant expression cassette comprising a polynucleotide whose expression, alone and in combination with additional polynucleotides, alters the number, type and configuration of aleurone cells within seed, (the polynucleotide is operably linked to a promoter). The method is useful for altering seed characteristics to produce a transgenic having seeds and grains with improved nutritional, industrial and agricultural traits. The present sequence is maize DEK1 from B73, which was used to illustrate the invention. The DEK1 protein is involved in aleurone cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Length 2159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jung R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                          1708. .2013
/label= Cystein_proteinase_domain_II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen B, Lid SE, L
Lorentzen JA, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.5%; Score 60; DB 56.2%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Page 105-109; 171pp; English
                                                                                                 ABP70924 standard; protein; 2159 AA.
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001; 2001US-0309719P.
25-OCT-2001; 2001US-0337444P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 WSLWALGWRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2002; 2002WO-US024438
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 WVLWAVNWRPWRLYSW
                                                                                                                                                             (first entry)
3 WSLWALGWRWLRRYGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                           28 WILWAVNWRPWRLYSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tarczynski MC, Olsen O,
Ananiev E, Nichols SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-248094/24.
                                                                                                                                                                                         Maize DEK1 from B73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells within seed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACC42659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation
                                                                                                                                                                                                                                                                                                                                                      WO2003011015-A2
                                                                                                                                                          26-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                ABP70924;
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                                                                       RESULT 10
                                                                                     ABP70924
ID ABP
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2000US-0249212P.
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17-NOV-2000;
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                                                                                                         Novel human respiratory antigen #177
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2000US-018062BP.
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2000US-0232080P
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28-JUN-2000, 2

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RESULT 11
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of novel human respiratory antigens, and cDNA (AAS27869-AAS28159) and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the tespiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders and cancers of the respiratory tissues e.g. pneumonia, allergic polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAUT/865-AAUT/975 represent novel human respiratory antisense therapy. AAUT/865-AAUT/975 represent novel human respiratory antisense therapy. ALU-869-dence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human respiratory system associated polynucleotide; respiratory system disorder; throat disorder; vocal cord paralysis; tonsillitis; laryngitis; lung disorder; pneumonia; allergic disorder; asthma; cosinophilic pneumonia; pleurisy; cystic fibrosis; emphysema; histiocytosis; sarcoidosis; nose disorder; rhinitis; sinusitis; neoplasm; cancer; respiratory tissue cancer; throat cancer; lung cancer; cancer of the nose; gene therapy; chromosome identification; forensic;
                                                                                                                                                                                                                                                                                                             Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis.
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Best Local Similarity 47.1%; Pred. No. 2.4;
Matches 8; Conservative 3; Mismatches 6; Indels
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   2000US-0250160P.
2000US-0250391P.
2000US-0251030P.
                                            2000US-0251988P.
2000US-0256719P.
2000US-0251479P.
2000US-0251856P.
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2000US-0251989P.
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2000US-0254097P.
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                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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N-PSDB; AAS28045.
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acid sequence that is at least 90% identical to polypeptide fragment of any one of 299 respiratory system antigen sequences (PS) and having biological activity, polypeptide domain or epitope of RS, full-length protein of PS, or variant, allelic variant or species homolog of PS. (I) protein of PS, or variant, allelic variant or species homolog of PS. (I) or a polymucleotide (II) encoding (I) is also useful for diagnosing a certain produced condition or a usceptibility to a pathological condition in a subject which involves determining the presence or absence of mutation in (II) or determining the presence or amount of expression of (I) in a biological sample and diagnosing a pathological condition based on the result. The human respiratory system associated polymucleotides, the polypeptides encoded by them, and antibodies that immunospecifically bind these polypeptides are useful in diagnosis, treatment, prevention and/or prognosis of disorders of respiratory system such as throat disorders (e.g., vocal cord paralysis, tonsillitis, and laryngitis), lung disorders (e.g., pneumonia), plantisy, cystic fibrosis, emphysema, histicoytosis, concerned is ancerned cancer, lung cancer, and cancer of the nose). The polymucleotides are useful in gene therapy
                                                                                                                                                                                                                                                                    The invention describes an isolated polypeptide (I) comprising an amino
                                                                                                                                           Novel respiratory system antigen and polynucleotides encoding the polypeptides, useful for treating diagnosing, treating or preventing tonsillitis, pneumonia, asthma and cystic fibrosis, emphysema, throat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%; Score 59; DB 7; Length 73; 47.1%; Pred. No. 2.4; 5; Wismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
(GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 479; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyanophage S-2L encoded protein #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG22291 standard; protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45...
47.18; PLL
                                                      Barash SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VWSLWALGWRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 IWSMWLPGEQWLRPXSW 32
                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2002; 2002FR-00005424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 47.1 tes 8; Conservative
                                                      Ruben SM,
                                                                                        WPI; 2003-902033/82
                                                                                                        N-PSDB; ADG40949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyanophage S-2L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2003
                                                   Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG22291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                  cancer,
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Matches
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Pochet S;

Galisson F, Bouzon M, Robert C, Vico V;

Kaminski PA, 7, Saurin W,

Marliere P, Ka Weissenbach J,

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Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics,
                                         New genomic sequence for cyanophage S-2L, useful for identifying genes for synthesis of 2,6-diaminopurine bases or polynucleotides containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 25051; 455pp; English.
                                                                                  Claim 6; SEQ ID NO 37; 423pp; French
                                                                                                                                                                                                                                                                                                                                                                                               ABO76305 standard; protein; 1086 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00252991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0074788P
98US-0094190P
                                                                                                                                                                                                                                                                          43.4%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
           2004-045746/05.
                                                                                                                                                                                                                                                                                                                     9 GWRWLRRYGW
                                                                                                                                                                                                                                                                                                                                          112 GWRWCRRGGW
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABD09876
                    N-PSDB; ADG22255
                                                                                                                                                                                                                                                     Sequence 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1999;
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Drmanac RT, Liu C,
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                                                                                                                                                                                      Local Similarity
nes 10; Conserv
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                                                                                                            Sequence 1086 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                         52
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                                                                                                                                                                Query Match
                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                             ABG18132
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The invention relates to the entire genome of cyanophage S-2L, and to the protein encoded by it. Genes isolated from the genome of S-2L are useful for preparing enzymes for synthesis of D-bases (D = 2,6-diaminopurine), particularly D, dDMP and dDTP, or polymucleotides containing these bases, polymerases involved in metabolism of D-bases and deoxymucleotide can long for detection and/or identification of S-2L, and for identifying agents that modulate synthesis of D-bases or polymucleotides containing them, and fusions of S-2L polypeptides with an antigen can be used to raise specific antibodies, useful for detecting S-2L. This sequence corresponds to one of the proteins encoded by the cyanophage S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 8; Length 122;
Pred. No. 9.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa polypeptide #8480.
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prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa mucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis andor treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                                                                                                                                  43.4%; Score 56; DB 7; Length 1086; 62.5%; Pred. No. 85; 2; Indels cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 48491; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #18123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG18132 standard; protein; 599 AA.
                                                                                                                                                                                                                                                                 segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         3 WSLWALGWRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
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CC of sites expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The polypeptide and polynuclocide sequences have applications in diagnostics, forenaics, gene mapping, identification of mutations of responsible for genetic disorders or other traits to assess biodiversity or and to produce other types of data and products dependent on DNA and common acid sequences of the invention. Note: The sequence data for this control amino acid sequences of the invention. Note: The sequence data for this control of commat directly from WIPO at control of commat directly from WIPO at control of format directly from WIPO at control of format directly from WIPO at control of format directly from WIPO at control of commat directly from WIPO at control of format directly from WIPO at conservative li Mismatches 5; Indels 0; Gaps 0; watches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0; but 171 SVEKLGWWERRYGW 185
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Search completed: October 26, 2004, 06:45:08 Job time : 86.5 secs

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Query Match
100.0%; Score 129; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-504-538A-12
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STATE: M.
COUNTRY:
                   46.5
46.5
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                                                                      Sequence 12, Appl
Sequence 12, Appl
Sequence 25051, A
Sequence 22986, A
Sequence 32165, A
Sequence 44, Appl
Sequence 10, Appl
Sequence 110, Appl
Sequence 31085, A
Sequence 298, App
Sequence 298, App
Sequence 298, App
Sequence 298, App
Sequence 2665, A
Sequence 16, Appl
Sequence 28405, A
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Sequence 9146, Ap
Sequence 12110, A
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                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                         // Search time 22 Seconds
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60.289 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/AB_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-32165
US-08-09-587-44
US-09-560-386A-10
US-09-252-991A-31470
US-09-252-991A-31085
US-09-38-352-6190
US-09-38-352-6190
US-08-637-558-298
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US-09-270-767-36409
US-09-270-767-51626
US-09-252-991A-19128
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US-09-270-767-31648
US-09-270-767-46865
US-09-247-890-16
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US-09-489-039A-9146
US-09-489-039A-12110
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US-09-252-991A-25051
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                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-724-969-16
US-09-724-852-16
                                                                                                                                                                        478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                          2004, 06:20:00 ;
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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
                                                                                                                      1 QVWSLWALGWRWLRRYGWNM 20
                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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129
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         Copyright
                                                          October 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                   Title:
Perfect score:
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47.5
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17896, A
17567, A
7878, Ap
26967, A
26696, A
                                                                             10, Appl
35, Appl
45, Appl
14865, A
14, Appl
16, Appl
16, Appl
29, Appl
29, Appl
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                                     Sequence 269
Sequence 266
Sequence 8,
Sequence 10,
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Sequence 4:
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                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08504538A
Sequence 12, Application US/08504538A
Sequence 12, Application US/08504538A
Septicant information:
APPLICANT: Brent, Roger
APPLICANT: Gessen, Timm H.
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING TITLE OF INVENTION: PROTEIN INTERACTIONS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110-2214
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC COMPATIBLE
COMPUTER: PATENTY BY PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/504,538A
FILING DATE: 07/20/95
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/278,082
FILING DATE: 07/20/94
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
PREGISTRATION NUMBER: 30,062
US-09-252-991A-17896
US-09-252-991A-17567
US-09-252-991A-26967
US-09-252-991A-26967
US-09-252-991A-26696
US-08-935-886-18
US-08-935-886-18
US-08-935-886-18
US-08-935-886-18
US-08-9280-590A-5
US-09-280-590A-5
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US-09-892-80-590A-16
US-09-892-80-590A-29
US-09-892-80-590A-29
                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Clark & Elbing
176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617) 428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  Massachusetts
  ADDANA
STREET: 1,0
TTW: Boston
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US-08-504-538A-12
    2226666666666444444
2001264566666444444
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Gaps

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Length 20; Indels

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| Sequence 25051, Application US/09252991A | Patent No. 655179A | Patent No. 655179A | Patent No. 655179A | Patent No. 7 | TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS | TITLE OF INVENTION: NUMBER: US/09/252,991A | TITLE OF INVENTION: NUMBER: US/09/252,991A | CURRENT FILING DATE: 1999-02-18 | PRIOR PRILOR APPLICATION NUMBER: US 60/074,788 | PRIOR PILING DATE: 1999-02-18 | PRIOR PILING DATE: 1999-02-18 | PRIOR PILING DATE: 1999-02-18 | PRIOR FILING DATE: 1998-07-27 | PRIOR FILING DATE: 1998-07-27 | SEQ ID NO. 25051 | LENGTH: 1086 | LENGTH: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.4%; Score 56; DB 4; Length 1086; 62.5%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 129; DB 5;
100.0%; Pred. No. 1.5e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00786/288001
                                                                                                                                                                                                                                                                                              SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09307
                                             Fish & Richardson, P.C.
                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVWSLWALGWRWLRRYGWNM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25051
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OVWSLWALGWRWLRRYGWNM
                                                                   225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WSLWALGWRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 62.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                              STATE: Massachusetts
COUNTRY: USA
                                                                                                                                      COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                           Boston
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                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-09307-12
                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ropology:
                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
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                                                                                                                                                                                                                        APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jessen, Timm H.
APPLICANT: Xu, Canxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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100.0%; Score 129; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,052
FILING DATE:
CLASSIFICATION NUMBER: US/08/630,052
FILING DATE:
CLASSIFICATION NUMBER: 08/504,538
FILING APPLICATION NUMBER: 08/504,538
FILING DATE: Unly 20, 1995
APPLICATION NUMBER: 08/278,082
FILING DATE: Unly 20, 1994
ATTORNEY/AGENT INPORMATION:
NAME: Karen F. Lech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jessen, Timm H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR
TITLE OF INVENTION: DETECTING PROTEIN INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/311001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application PC/TUS9509307 GENERAL INFORMATION:
                                                                                                                                      US-08-630-052-12; Sequence 12, Application US/08630052; Patent No. 6399296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OVWSLWALGWRWLRRYGWNM 20
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    OVWSLWALGWRWLRRYGWNM 20
                                             OVWSLWALGWRWLRRYGWNM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 542-5070
(617) 542-8906
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPN
                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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PCT-US95-09307-12
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US-08-630-052-12
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Length 20;

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                                                                                               AND
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APPLICANT: GETTIG, RUSSELL R.
APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETTI, ENCO.
APPLICANT: PROJECTIT, ENCO.
APPLICANT: PROJECTIT, STEVEN E.
TITLE OF INVENTION: WECTORS HAVING ENHANCED EXPRESSION,
TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/09079587

Patent No. 6130066
GENERAL INFORMATION:
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIC, RUSSLL R.
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN B.
TITLE OF INVENTION: WECTORE HAVING ENHANCED EXPRESSION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                        ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,155B
FILING DATE: 12-MAR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 2;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                          FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454310-2990
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGIESTRATION NUMBER: 32,443
REFERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 550 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                  745 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             745 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 550 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 WRWGWRWLHQY 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: FROMMER LAN
STREET: 745 FIFTH AVE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 WALGWRWLRRY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10151
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: n/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEW YORK
                                                                                                                                                                                                                                         CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-816-155B-44
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US-09-079-587-44
                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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APPLICANT: MARC J. RUBERFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
RAIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32165
LENGTH: 382
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MAC J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: 0590/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22986
LENGTH: 260
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41.1%; Score 53; DB 4; Length 260;
Best Local Similarity 45.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32165, Application US/09252991A Patent No. 6551795
                                                                                                    RESULT 5
US-002-252-991A-22986
; Sequence 22986, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-816-155B-44
Sequence 44, Application US/08816155B
Patent No. 5990091
GENERAL INFORMATION:
APPLICANT: TARTAGLIA, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 VWSGWILAHETRWDWVGQLGW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VWSLWALG----WRWLRRYGW 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 VWLHRLAHGLWTSGWKWLAR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TARTAGLIA, JAMES APPLICANT: COX, WILLIAM I.
       52 WSRWA----WLRRNGW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-252-991A-32165
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GENERAL INCRMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                 39.5%; Score 51; DB 4; Length 480; ilarity 100.0%; Pred. No. 79; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.8%; Score 50; DB 4; Length 266; Best Local Similarity 45.0%; Pred. No. 59; Matches 9; Conservative 0; Mismatches 7; Indels
  JMBER: US 60/094,190
1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 31085, Application US/09252991A ; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6190, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 VWAAGVFVAFQEWGWLGRLGW 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LWALG------WRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 WSLWALG----WRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31085
                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331.
SEQ ID NO 31470
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                          255 LGWRWLRR 262
                                                                                                                                                                                                                                                                                                              8 LGWRWLRR 15
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                       US-09-252-991A-31470
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-31085
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                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLS OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLS REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRICR APPLICATION NUMBER: US 60/074,788
PRICR FILLING DATE: 1999-02-18
PRICR FILLING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 3; Length 550;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                        PLICALION NUMBER: US/09/07,587

CLASSIPICATION
PRIOR APPLICATION
PRIOR APPLICATION
APPLICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-MAR-1997
ATTONREY/ABGNT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REGISTRATION NUMBER: 454310-2990
TELEPHONE: 212-588-0500
TELEFRAX. 212-588-0500
TELEFRAX. 212-588-0500
TELEFRAX. 212-588-0500
TELEFRAX. 550 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: n/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Boutand, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
                                              APPLICATION NUMBER: US/09/079,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09560385A Patent No. 6703363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-09-079-587-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 WRWGWRWLHQY 536
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US-09-252-991A-31470
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Gaps

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Gaps

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC COMPATIBLE
COMPUTER: THE PC COMPATIBLE
COMPUTER: THE PC COMPATIBLE
COMPUTER: DEADER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-UN-1997
CLASSIFICATION 0ATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PADST, PATENE L.
REGISTRATION: WUMBER: 31,284
REGISTRATION NUMBER: RPMS 101 CON
TELEPHONE: (404) 873-873
TELEPHONE: (404) 873-873
TELEPHONE: (404) 873-873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IDEA COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabet
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 3;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
RESISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-201-945-298
; Sequence 298, Application US/09201945
; Patent No. 6342215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 298:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.0%;
50.0%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 WSLWALGWRWLRRY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 WELLSLNWRWYFRF 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 61 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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Pred. No. 19;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION 435

PRIOR APPLICATION DATE:

PRIOR APPLICATION NUMBER:

PULING DATE:

LOBEC-1995

CLASSIFICATION:

APPLICATION:

APPLICATION:

APPLICATION:

APPLICATION:

APPLICATION:

NAME:

REFERENCE POCKET NUMBER:

REFERENCE/DOCKET NUMBER:

REFERENCE/DOCKET NUMBER:

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION:

TOTAL APPLICATION

TOTAL APPLIC
                                                                                                                                          Sequence 298, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT DAVID William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 299. Application US/08871355A
Patent No. 601569
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Gen
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CONTY: ALLanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
48 WSWWRRTRRRLWRWWRRLRW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 298
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.0%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 WELLSLNWRWYFRF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0°
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-871-355A-298
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                                                                                               RESULT 13
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Gaps

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Length 61; 5; Indels

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| TELECOMMUNICATION INFORMATION:
| TELEPHONE: (404) 873-8794 |
| TELEPAX: (404) 873-8795 |
| TELEFAX: (404) 873-8795 |
| TELEFAX: (404) 873-8795 |
| INFORMATION FOR SEQ ID NO: 298:
| SEQUENCE CHARACTERISTICS: |
| TEMPOLY: animo acids |
| TOPOLOGY: Inear |
| MOLECULE TYPE: protein |
| HYPOTHETICAL: NO |
| WS-09-201-945-298 |
| Query Match |
| Best Local Similarity | 50.0%; Pred: No: 19; Pred:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 26, 2004, 06:19:49; Search time 17 Seconds (without alignments) 113.196 Million cell updates/sec

US-10-066-965A-1 Perfect score: Title:

129 1 QVWSLWALGWRWLRRYGWNM 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote			G	probable alkane hy	hypothetical prote			hypothetical prote	conserved hypothet	env polyprotein pr	type IV prepilin p	hypothetical prote	melittin resistand	phosphate transpor	surface antigen -	probable membrane	hypothetical prote	middle surface ant	conserved hypothet	hypothetical prote	large surface anti	large surface anti			large surface anti	-xylo	rhodopsin, long-wa	
SUMMARIES	ID	G96595	17	S74708	A83169	B83454	T15209	B83755	W4BP77	C83311	A83325	G46335	C53374	AD2430	AB3647	B70584	I48192	S61624	H75284	SAVL64	AH2931	F98350	SAVLC	SAVLS	SAVL59	SAVL7	SAVLW8	D90483	JC4933	C69432
	DB	. 2	7	7	~	ď	C)	€	Н	~	7	Н	C)	N	~	7	~	~	7	-	7	7	Н	Н	П	Н	П	7	7	C
	* Query Match Length	2143	847	485	258	377	411	795	135	297	382	990	102	167	477	305	123	191	165	282	389	425	426	428	431	431	431	731	377	227
d	% Query Match	46.5	45.7	45.0	41.1	41.1	41.1	41.1	39.5	σ	σ	9	æ	æ	38.8	80	œ	ω ω	8	œ		ω.		38.0	æ			38.0		
	Score	09	59	58	53	53	53	53	51	51	ö	50.5	20	20	50	49.5	49	49	49	49	49	49	49	49	49	49	49	49	48.5	48
	Result No.	; ; ; ; ;	7	ю	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	nucleoprotein - in	glucose-triggered	hypothetical prote	probable transport	opsin, ocellar - A	opsin, lateral eye	hypothetical prote	hypothetical prote	hypothetical prote	probable sugar upt	phage protein homo	GumG protein - Xan	probable transport	hypothetical prote
T20486	F72335	VHVNIH	T41125	AG2839	A97617	A48197	B48197	G72226	D82590	D83210	A95971	AI1590	S67856	G83043	B70709
7	7	Т	7	Ŋ	7	7	7	N	~	7	(7)	(1)	7	7	7
287	398	413	466	504	518	376	376	71	201	266	275	278	379	453	540
37.2	37.2	37.2	37.2	37.2	37.2	36.8	36.8	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4
48	48	48	48	48	48	47.5	47.5	47	47	47	47	47	47	47	47
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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hypothetical protein F7A10.23 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Spacession: G96595 (Mour-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 (Spacession: G96595 Mour-2001 Mour-2001 Mouse, 
G96595
```

A;Gene: F7A10.23 A;Map position: 1

Gaps .; 0 Length 2143; Indels ; Score 60; DB 2; Pred. No. 10; 1; Mismatches 46.5%; 56.2%; Query Match
Best Local Similarity 56.2³
Matches 9; Conservative

ö

3 WSLWALGWRWLRRYGW 18 28 WILWAVNWRPWRLYSW 43 dd δ

RESULT 2 T04772

hypothetical protein F10M10.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004
C;Accession: T04772
R;Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mewes, H.W.; Mayer,
R;Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mewes, H.W.; Mayer,
R;Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mewes, H.W.; Mayer,
R;Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mewes, H.W.; Mayer,
R;Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mayer,
R;Bevan, M.; De Haan, M.; Mayer, Mayer,
R;Molecule type. DNA
A;Residues: 1-847 cBEV>
A;Cross-references: UNIPROT:Q9SYZI; EMBL:AL035521
A;Experimental source: cultivar Columbia; BAC clone F10M10
C;Genetics:
A;Map position: 4
A;Introns: 91/1; 139/3; 416/1; 475/3; 528/3; 603/3; 603/1; 748/2

à g

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probable alkane hydroxylase PAL525 [imported] - Pseudomonas aeruginosa (strain PAO1) ("Species: Pseudomonas aeruginosa C.Species: Pseudomonas aeruginosa C.Species: Dsep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004 ("Accession: BB3454 ("Accession: BB3454 ("A.S.") "Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                            A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho **Reference number: A82950; MUID:20437337; PMID:10984043
A,Accession: B83454
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1-377 <STO>
A,Cross-references: UNIPROT:Q91318; GB:AE004581; GB:AE004091; NID:g9947482; PIDN:AAG0491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:001815; EMBL:AP003141; NID:g2088732; PID:g2088734; PIDN:AAB5
A;Experimental source: strain Bristol N2; clone W02D3
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: B83755
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Caenorhabditis elegans
Cibate: 20-8ep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cibacession: T12209
Rice, T.; Weinstock, L.; Rifkin, L.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid W02D3.
A;Reference number: Z18308
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C.Accession: B83755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BH0842 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 42.9%; Pred. No. 15; 9; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein W02D3.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53; DB 2;
Pred. No. 16;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 VWSGWILAHETRWDWVGQLGW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VWSLWALG----WRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: CESP:W02D3.2
A;Map position: 1
A:Introns: 202/2; 334/2; 359/2
C;Superfamily: dibydroorotate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: PA1525
C;Superfamily: Alkane 1-monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 WSLWALGWRWLRRYGWN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 47.1%; 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 WAVRAASWGLLPRFGWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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C;Species: Pseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Dseudomonas aeruginosa
C;Species: Species: Osporomonas aeruginosa
C;Species: Species: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
S74708
bypotein slr1306 - Synechocystis sp. (strain PCC 6803)
c)Species: Synechocystis sp.
A,Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74708
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74708
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74708
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Asneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Reference number: S74322; MUID:97061201; PMID:8905231
A.Recession: S74708
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-485 < KAN>
A.Residues: 1-485 < KAN>
A.Residues: UNIPROT:P72844; EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA1685
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                ..
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A;Note: F10M10.30
C;Superfamily: Arabidopsis thaliana hypothetical protein F10M10.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.0%; Score 58; DB 2; Length 485; Best Local Similarity 50.0%; Pred. No. 4.4; Matches 10; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
Local Similarity 45.0%; Pred, No. 10;
68 9; Conservative 1; Mismatches 4; Indels
                                                                                                                       DB 2; Length 847; 5.7;
                                                                                                                       Score 59; DB Pred. No. 5.7; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 WSLWALG-----WRWLRRY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VW----SLWALGWRWLRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 WGLWALSGLGLVIWRWRRH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 VWLHRLAHGLWTSGWKWLAR 54
                                                                                                                                                                                                                                                                                                                                                            503 VWALWPMGGAWLCTHAW 519
                                                                                                                                                                                                                                                                                        2 VWSLWALGWRWLRRYGW 18
                                                                                                                       Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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RESULT 4

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A; Reference number: A94615 A; Accession: A04411 A; Molecule type: DNA A; Residues: 1-135 < DUN>

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C;Superfamily: visna lentivirus type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein
F;101-662/Product: exterior membrane glycoprotein #status predicted <EXT>
F;663-699/Product: exterior membrane glycoprotein #status predicted <TMM'>
F;663-689/Region: hydrophobic
F;842-863/Domain: transmembrane #status predicted <TMM'>
F;141,162,207,259,299,363,386,402,413,434,438,469,474,480,490,500,514,526,536,542,550,566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: G46335
R;Querat, G.; Audoly, G.; Sonigo, P.; Vigne, R.
R;Querat, T.5, 434-447, 1990
A;Title: Nucleotide sequence analysis of SA-OMVV, a visna-related ovine lentivirus: phylocalyReference number: A46335; MUID:90223989; PMID:2158181
                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein PA2574 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-5ep-2000 #sequence_revision 15-5ep-2000 #text_change 16-Aug-2004
C;Accession: A83325
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A,Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-382 <STO>
A;Cross-references: UNIPROT.Q910R2; GB:AE004685; GB:AE004091; NID:g9948627; PIDN:AAG05962
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                        0;
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C,Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A,Residues: 1-990 <QUE>
A,Cross-references: GB:M31646; NID:g808756; PIDN:AAA66817.1; PID:g332551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             env polyprotein precursor - Maedi/Visna virus (strain SA-OMVV)
N;Alternate names: coat polyprotein
N;Contains: exterior membrane glycoprotein; transmembrane glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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   Length 297;
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Pred. No. 76;
2; Mismatches 7;
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39.5%; Score 51; DB 2; 100.0%; Pred. No. 21;
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Pred. No. 31;
1; Mismatches
                                                              0; Mismatches
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C;Superfamily: Alkane 1-monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.1%;
milarity 42.9%;
Conservative 1
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1 Similarity 27.8%;
10; Conservative 5
                                                              Conservative
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Best Local Similarity
9; Conserve
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Best Local Similarity
Matches 10; Conserv
      Query Match
Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
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S;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, D.; Hickey, M.J.; Bradan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A;Reference number: A882950; MUID:20437337; PMID:10984043
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A;Cross-references: UNIPROT:Q910H7; GB:AE004695; GB:AE004091; NID:g9948730; PIDN:AAG0604
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2661
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                                     A;Residues: 1-795 <STO>
A;Cross-references: UNIPROT:Q9KELO; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB045
A;Cross-references: strain C-125
C;Genetics:
A;Gene: BH0842
C;Superfamily: Arabidopsis thaliana hypothetical protein F10M10.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P03786
R;Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A;Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Accession: S42310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene 4.7 protein - phage T7
C;Species: phage T7
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 135,
                                                                                                                                                                                                                                                 Query Match 41.1%; Score 53; DB 2; Length 795; Best Local Similarity 41.2%; Pred. No. 30; Matches 7; Conservative 4; Mismatches 6; Indels
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Indels

Score 51; DB 1 Pred. No. 9.9; 1; Mismatches

39.5%;

Query Match 39.5 Best Local Similarity 63.6 Matches 7; Conservative

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A,Accession: C83311 A,Status: preliminary A,Molecule type: DNA

A,Map position: 34.87-35.88 C,Superfamily: phage T7 gene 4.7 protein

A; Molecule type: DNA A; Residues: 1-135 < DUW>

C.Genetics:

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Gaps

0;

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A,Molecule type: DNA
A,Residues: 1-477 <KUR>
A;Cross-references: UNIPROT:Q8YB02; GB:AE008918; PIDN:AAL54341.1; PID:g17985322; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphate transport system permease protein A-1 - Mycobacterium tuberculosis (strain H371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nylternate names: psfal protein
(Species: Mycobacterium tuberculosis
(Species: Mycobacterium tuberculosis
(Species: Mycobacterium tuberculosis
(Species: Nycobacterium tuberculosis
(Spacies: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 09-Jul-2004
(Spacies: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 09-Jul-2004
(Spacies: S. T.) Brosch, R.; Parkhill, J.; Garnier, T.; Ghurcher, C.; Hanris, D.; Gordon, S.; Connor, R.; Davies, R.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. A; Hatter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
A; Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:086345; GB:Z95209; GB:AL123456; NID:g3261750; PIDN:CAB08490.
A,Experimental source: strain H37Rv
R;Braibant, M.; De Mit, L.; Peirs, P.; Kalai, M.; Ooms, J.; Drowart, A.; Huygen, K.; Con submitted to the EMBL Data Library, December 1996
A,Description: Structure of the Mycobacterium tuberculosis Antigen 88, a protein related A,Reference number: S78423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 'MTVLPYGRSGVVAASMLGLGRALGETVAVL','VILRSAGAAGDLVAVRRRLYVRRQDRLRCF','RIQRTAADRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-4,'T',6-207,'A',209-304 <BRA>
A;Cross-references: EMBL:X75297; NID:g1182012; PIDN:CAA53045.1; PID:g1182013
A;Note: this is a revision to the sequence from reference S42804
B;Content, J.
Submitted to the EMBL Data Library, September 1993
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44;
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Pred. No. 33;
1; Mismatches
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Pred. No.
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Job time : 18 secs
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47.1%; Pred
1; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 VWMLWRGNWRDLKHLPW 203
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                                                                                                                                                                                                   A:Experimental source: strain 16M
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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Best Local Similarity
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                                                     A;Status: preliminary
                   A;Accession: AB3647
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A;Gene: BMEII1099
A;Map position: II
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                                                                                                                                                                type 1V prepilin peptidase (EC 3.4.99.-) pilD - Neisseria lactamica (strain LNP411) (fra N; Contains: type IV pilin N-methyltransferase (EC 2.1.1.-)
(Species: Neisseria lactamica (Signate: 22-13n-1995 #sequence_revision 23-Mar-1995 #text_change 29-Jan-1999 (Spacession: CS3374 #sequence_revision 23-Mar-1995 #text_change 29-Jan-1999 (Spacession: CS3374 * Pugsley, A.P. U. B. Pugsley, A.P. U. B. Pugsley, A.P. U. B. Pugsley, A.P. U. Pateraiol. 176, 133-1331, 1994 (A) Title: Type IV prepilin peptidase gene of Neisseria gonorrhoeae MS11: presence of a re A; Reference number: A53374; MUID: 94156836; PMID: 7906688 (A) Residues: Dreliminary; nucleic acid sequence not shown; not compared with conceptual tra A; Molecule type: DNA (A) Residues: 1-102 and A; Residues: 1-103 and A; Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein alr4996 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Notes Nostoc sp. PCC 7120
A;Notes Nostoc sp. Strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2430
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. B, 205-213, 2001
A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-167 < KUR,
A;Residues: 1-167 < KUR,
A;Residues: 1-167 < KUR,
A;Reperimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4996
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
J; Mazur, M.; Goltsman, E.; Selkov, E.; Bizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
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2; Mismatches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                            - protein search, using sw model
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32 53 41.1 374 2 Q8P451 Q6B9451 xanthomonas 34 53 41.1 377 2 Q6H927 Q6H927 Q6h927 pseudomonas 34 53 41.1 377 2 Q6H927 Q6h927 pseudomonas 35 53 41.1 377 2 Q6H941 pseudomonas 37 53 41.1 377 2 Q6H941 pseudomonas 37 53 41.1 2 C01118 C011
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TAXID=7227;
                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.5%; Score 69; DB 2; Length 258;
56.2%; Pred. No. 0.37;
cive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Akopiants K.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U24442; AAB03856.1; -.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR002575; APH trans.
InterPro; IPR011009; Kināse_like.
InterPro; IPR008566; Tyr_pkinase_AS.
near. PR01856; APH; 1.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Akopiants K.E., Danilenko V.N.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 AA; 28490 MW; D2AD3F681470264E CRC64;
                                                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Aminoglycoside-O-phosphotransferase type 5.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01636; APH; 1. ___
PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
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  258 AA
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                                                    (TrEMBLrel. 01, (TrEMBLrel. 01,
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PIR; G96595; G96595.
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nes 9; Conservative
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MEROPS; C02.019; -.
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
             SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
FINEL, BT001327; AAN71082.1; --
FINEL, BT001327; AAN71082.1; --
FINELS EMBL SA, 20300 MW; 927D2F2060330C99 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).
Wkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Park Y.-J., Rostoks N., Ramakrishna W., SanMiguel P., Shiloff
Ma J., Jiang Z., Kleinhofs A., Bennetzen J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF480496; AAL87147.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.5%; Score 60; DB 2; Length 156; 56.2%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                          Score 61; DB 2; Length 162;
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 AA; 18241 MW; OE8A04B23AA15BA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence upd
01-MRA-2003 (TrEMBLrel. 23, Last annotation up
Putative n-calpain-1 large subunit (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA
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                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative n-calpain-1 large subunit. Name=49D11.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||:|: | || || || || || 51 MWSMWSRRWNRRSRWN 72
                                                                                                                                                                                                                                                                                                                                                                                                                               2 VWSLWALGW ---- RWLRRYGWN 19
                                                                                                                                                                                                                                                                                                                        / Match 47.3%;
Local Similarity 45.5%;
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 WSLWALGWRWLRRYGW 18
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nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                             Query Match
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Q8S3T1
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Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Koning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                              Length 543;
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SMART; SM00230; CysPc; 1.
PROSITE; PS50203; CALPAIN CAT; 1.
PROSITE; PS01039; THIOL PROTEASE CYS; 1.
SEQUENCE 2143 AA; 236779 MW; B91A15081AF26EC2 CRC64;
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                                                            Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W Theologis A.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AVS50822, AAK92757.1; -.
NON TER 543
SEQÜENCE 543 AA, 59467 MW, FB988FE03FD3AD48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Town C.D., Kaul S.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004198; F:calpain activity; IEA.
GO; GO:0005198; F:calpain activity; IEA.
INTERP. IPRO01300; Peptidase C2.
InterPro; IPRO01300; Peptidase C2.
Fam; PRO1067; Calpain_III; 1.
PERN; PRO0648; Peptidase C2; 1.
PRINTS; PRO0704; CALPAIN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
N-calpain-1 large subunit, putative; 13921-23959.
                                                                                                                                                                                                                                                                        46.5%; Score 60; DB 2; 56.2%; Pred. No. 11; ttive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.5%; Score 60; DB 2;
56.2%; Pred. No. 41;
iive 1; Mismatches
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Arabidopsis thaliana (Mouse-ear cress).
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Gaps

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Length 2159;

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R GO; GO:0005622; C:intracellular; IEA.

GO; GO:0004199; F:calpain activity; IEA.

R GO; GO:0004199; F:calpain activity; IEA.

R InterPro; IPR008965; ConA like lec_gl.

R InterPro; IPR001300; Peptidase.C2.

R InterPro; IPR001300; Peptidase.C2.

R InterPro; IPR00169; Peptidase.C2.

R Pfam; PF00167; Calpain_III; 1.

R SMART; SM00720; Calpain_III; 1.

R SMART; SM00230; CAPE; 1.

R RSART; SM00230; CAPE; 1.

R PROSITE; PS50203; CALPAIN CAT; 1.

R PROSITE; PS00032; NG MTASE; UNKNOWN 1.

R PROSITE; PS00132; THIOL PROTEAGE CYS; 1.

SR PROSITE; PS0139; THIOL PROTEAGE CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 2159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.5%; Score 60; DB
56.2%; Pred. No. 41;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
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01-MAR-2004 (TrEMBLre
Calpain-like protein.
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Best Local Similarity
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nes 9; Conserv
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Matches
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                                                                                        Calpain-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                             When the control of the calpain gene required for aleurone cell development in the endosperm of maize grains encodes a membrane protein of the calpain gene superfamily.";

The control of the calpain gene superfamily.";

Expect Natl. Acad. Sci. U.S.A. 99:5460-5465 (2002).

Expect Natl. Acad. Sci. U
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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PubMed=11929961;
Lid S.E., Gruis D., Jung R., Lorentzen J.A., Ananiev E.,
Chamberlin M., Niu X., Meeley R., Nichols S., Olsen O.A.;
"The defective kernel 1 (dekl) gene required for aleurone cell
development in the endosperm of maize grains encodes a membrane
protein of the calpain gene superfamily.";
EMBL; AY061804; AAL38187.1; -.
EMBL; AY064805; AAL38187.1; -.
EMBL; AY064805; AAL38188.1; -.
HSSP; P17655; IKEX.
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        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Developing seed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calpain-like protein.
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                                                                                                                                                                                                                                                                                                                                                    PubMed=11929961;
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QBRUQ1
              DDT REAL PROPERTY OF A REAL PROP
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Developing endosperm, PubMed=11929961; bid S.E., Gruis D., Jung R., Iorentzen J.A., Ananiev E., Chamberlin M., Niu X., Meeley R., Nichols S., Olsen O.A.; chamberlin M., Niu X., Meeley R., Nichols S., Olsen O.A.; with defective kernel I (dekI) gene required for aleurone cell development in the endosperm of maize grains encodes a membrane protein of the calpain gene superfamily."; broc. Natl. Acad. Sci. U.S.A. 99:5460-5465(2002). EMBI, AYOGA 806, AAL38189.1; -.
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PROSITE; PS00092; N6 MTASE; UNKNOWN 1.
PROSITE; PS00139; THIOL, PROTEASE CYS; 1.
SEQUENCE 2159 AA; 238997 MW; 9F995D3F9EAC1315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMORS, CO.2.0.10; ...

GO; GO:0004198; F:calpan activity; IEA.

GO; GO:0004198; F:calpan activity; IEA.

GO; GO:0004198; F:calpan activity; IEA.

GO; GO:0006208; P:calpan activity; IEA.

InterPro; IPR008985; ConA like_lec_gl.

InterPro; IPR0010505; No.Merase.

InterPro; IPR00101300; Pepticase C2.

InterPro; IPR001019; Pepticase C2.

R Pfam; PF00164; Calpain III; 1.

R Pfam; PF00648; Peptidase C2: 1.

R SMART; SM00720; Calpain_III; 1.

R SMART; SM00230; CysPc; 1.

R SMART; SM0230; CysPc; 1.
(TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.5%; Score 60; DB 2;
56.2%; Pred. No. 41;
ative 1; Mismatches
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Mus musculus (Mouse)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                     RESULT 11
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                                                                                                                                                Oryza sativā (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dekl-calpain-like protein.

OJ1311_H06.4.

OJ1311_H06.4.

OYza Sativa (japonica cultivar-group).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae;

Ehrhartoideae; Oryzeae, Oryza, Oryza sativa.
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STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Irya sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC "Irya sativa nipponbare(GA3) genomic GNA, chromosome 2, BAC olone:04131 H06";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                         A Sasaki T. Matsumuco T., Yamamoto K.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
E EMBL, APOO4161; BADO7761.1;
R InterPro; IPR001895; ConA like_lec_gl.
R InterPro; IPR001895; ConA like_lec_gl.
R InterPro; IPR001805; N6 Mtase.
R InterPro; IPR00180; Peptidase C2.
R InterPro; IPR00169; Peptidase C2.
R Pfam; PF01067; Calpain III; 1.
R Pfam; PF00648; Peptidase C2; 1.
R PRINTS; PR00704; CALPAIN.
R SMART; SM00720; CALPAIN.
R SMART; SM00230; CAPPAIN.
R SMART; SM00230; CAPPAIN.
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llarity 56.2%; Pred. No. 41;
Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2162;
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PROSITE; PS00092; NG MTASE; UNKNOWN 1.
PROSITE; PS00139; THIOL PROTEASE CYS; 1.
SEQUENCE 2162 AA; 239856 MW; 9FF44A8AE2B23F0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                 (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                     PRT; 2162 AA
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                                                                                           Created)
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          29 WVLWAVNWRPWRLYSW 44
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                                                                                          05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                          Dekl-calpain-like protein.
Name=0J1311_H06.4;
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Best Local Similarity 56.2
Matches 9; Conservative
                                                                    PRELIMINARY;
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Best Local Similarity
Matches 9; Conserv
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                                                                                                    05-JUL-2004
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                                                                              Q6ZFZ4;
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                                             RESULT 9
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SEQUENCE FROM N.A.
STRANT-GSTBLAG TISSUE=Bone;
STRANT-GSTBLAG TISSUE=Bone;
The FANTOM CONSORTIUM.
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
The RIKEN GENOME Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of G0,770 full-length CDNAs.";
Nature 420:563-573 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus adult male bone cDNA, RIKEN full-length enriched library,
clone:9830169C09 product:ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-TRNA LIGASE) (ALARS) homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayasus N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshika M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik integrated sequence analysis (RISA) system:384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                          164 AA
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=20499374; PubMed=11042159;
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WSLWALGWRWLRRYGW 18
                                                                                  44
                                                                              29 WILWAVNWRPWRLYSW
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Gaps
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                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thalīana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyra, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chang C.H., Dale J.M., Haysahizaki Y., Hasuan V.W., Land D., Jane J., Karlin-Neumann G., Kawai J., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Safou M., Seki M., Southwick A., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, BY102722, AAO11638.1;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017237, AE05266.1; -.
Hypothetical protein.
SEQUENCE 312 AA; 35001 MW; 577E4AE35A177103 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR008928; Glyco trans 6hp. 
SEQUENCE 843 AA; 93724 \overline{M}W; \overline{ZE}F1315DF98A1365 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein AT4934260.
                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                      DB 2;
8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.7%; Score 59; DB 2; 47.1%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                       843 AA
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Pred. No.
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                                                                                                                      45.7%;
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                                                                                                 Query Match
Best Local Similarity 50.00,
The B; Conservative
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Best Local Similarity
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Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki Y., Ohradaki K., Nomura K., Numazaki K., Ohradato M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                Gaps
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                   46.1%; Score 59.5; DB 2; Length 164; 58.8%; Pred. No. 4.2; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium paratuberculógis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.7%; Score 59; DB 2; Length 312; 50.0%; Pred. No. 8.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017237, AAS05266.1; -.
InterPro; IFR00123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
Complete Proteome; Hypothetical protein.
SEQUENCE 312 AA; 35001 MM; 577E4AE35A177103 CRC64;
                                                                                                                                                                                                                                D73DC68F0E60F610 CRC64;
                                                                                                                                            EMBL, AK036738; BAC29558.1; -.
GO; GO:0004813; F:alanine-tRNA ligase activity; IEA
GO; GO:0016874; F:ligase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium avium complex (MAC).
                                                                                                                                                                                                          Aminoacyl-tRNA synthetase; Ligase
SEOUENCE 164 AA; 18827 MW; D7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium paratuberculosis.
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Best Local Similarity 50.vv
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Best Local Similarity 58.8
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=k10;
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AAS05266;
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Q73VR3; Q73VR3

RESULT 12

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Q73VR3

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RESULT 13

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AAS05266

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0;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBJUBILITY
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503 VWALWPMGGAWLCTHAW 519
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Search completed: October 26, 2004, 06:39:20 Job time : 94 secs

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Sequence 1, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 187850,
Sequence 187850,
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 479, Appl
Sequence 479, Appl
Sequence 479, Appl
                                                                                                    October 26, 2004, 06:45:25; Search time 64.25 Seconds (without alignments) 100.781 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(gn2_6/ptodata/2/pubpaa/US07 PUBCCMB pep:*
(gn2_6/ptodata/2/pubpaa/US07 PUBCCMB pep:*
(gn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
(gn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
(gn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
(gn2_6/ptodata/2/pubpaa/US08 PUBCCMB.pep:*
(gn2_6/ptodata/2/pubpaa/US08 PUBCCMB.pep:*
(gn2_6/ptodata/2/pubpaa/US08 PUBCCMB.pep:*
(gn2_6/ptodata/2/pubpaa/US08 PUBCCMB.pep:*
(gn2_6/ptodata/2/pubpaa/US08 PUBCCMB.pep:*
(gn2_6/ptodata/2/pubpaa/US08 PUBCCMB.pep:*
(gn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*
(gn2_6/ptodata/2/pubpaa/US10B_PUBCCMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-162-538-12
US-10-066-95A-1
US-10-066-95A-7
US-10-066-95A-2
US-10-066-95A-8
US-10-437-963-187850
US-10-208-948-4
US-10-208-948-4
US-10-208-948-27
VS-10-208-948-24
US-10-208-948-24
US-10-74-095-479
US-09-764-860-479
US-09-764-860-479
US-10-74-095-479
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      1364641 segs, 323758627 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                          1 QVWSLWALGWRWLRRYGWNM 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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129
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Perfect score:
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                                                                                                              Run on:
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ALIGNMENTS

Sequence 44142, A Sequence 189763, Sequence 24744, A Sequence 203054, Sequence 142534, Sequence 11957, A Sequence 66556, A Sequence 5089, Ap Sequence 144606, Sequence 198121, Sequence 2277, A Sequence 2747, Ap Sequence 10, Appl Sequence 721, App Sequence 5052, A Sequence 5062, A 106350, 49338, A 52367, Sequence Seguence Sequence Sequence Sequence Sequence 5 US-10-424-599-149236 5 US-10-424-599-149236 5 US-10-424-599-189763 5 US-10-424-599-189763 5 US-10-424-599-189763 6 US-10-424-599-189763 7 US-00-425-11957 6 US-10-427-963-142534 6 US-10-427-963-14656 6 US-10-437-963-14666 6 US-10-437-963-198124 6 US-10-437-963-198124 6 US-10-437-963-198124 7 US-10-603-725-10 7 US-10-603-725-10 8 US-10-603-725-10 9 US-10-603-725-10 1 US-10-603-725-10 1 US-10-603-725-10 1 US-10-603-725-10 2 US-10-603-725-10 6 US-10-603-725-10 6 US-10-603-725-10 6 US-10-603-725-10 7 US-10-603-725-10 8 US-10-603-725-10 9 US-10-767-701-54428 1 US-10-767-701-54428 1 US-10-767-701-54428 1 US-10-767-701-54428 1 US-10-767-701-54428 1 US-10-767-701-54738 1 US-10-767-701-54738 1 US-10-369-493-15781 US-10-369-493-16163 4444444444444444444444

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RESULT 1

US-10-162-538-12

US-10-162-538-12

Sequence 12, Application US/10162538.

Publication No. US20030113749A1

GENERAL INFORMATION:

MCCOY, John M.

Jessen, Timm H.

Xu, Chanxing Wilson

TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING

PROTEIN

INTERACTIONS

NUMBER OF SEQUENCES: 28

CORRESPONDENCES: 28

CORRESPONDENCES: 128

COURTY: Bosch ADDRESS:

STATE: Massachusetts

COMPUTRY: USA

COMPUTRY: USA

COMPUTRY: USA

COMPUTRY: BASACHUSETE FORM:

MEDICATION TYPE: FLORPY disk

COMPUTRY: BASACHUSETE POOS/MS-DOS

SOFTWARE: PATENTIN SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN SYSTEM: US/10/162,538

FILING DATE: UNMOBER: US/10/162,538

FILING DATE: UJN, 20, 1995

FILING DATE: UJN, 20, 1995

APPLICATION NUMBER: 08/276,082

FILING DATE: UJN, 20, 1994

FILING DATE: UJN, 20, 1994
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0;

Gaps

0;

Indels

Length 20;

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; Sequence 2. Application US/10066965A; Publication No. US2030143626A1; Publication No. US2033143626A1; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: COLAS, PIERRE
; APPLICANT: COLEN, BARAK A.; TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS; FILE REFERENCE: EGGYP 3.0-015; FILE REFERENCE: EGGYP 3.0-015; CURRENT APPLICATION NUMBER: US/10/066,965A; CURRENT FILING DATE: 2002-12-09; NUMBER OF SEQ ID NOS: 33; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COLAS, PIERRE
APPLICANT: BEENT, ROGER
APPLICANT: BEENT, ROGER
APPLICANT: COHEN, BARAK A.

TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REPERBENCE: BGYPD 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILING DATE: 2002-12-09
NUMBER OF SRQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: peptide US-10-066-965A-8
                                                                 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-066-965A-2
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                                                                                                                                                                                        100.0%; Score 129; DB 14;
100.0%; Pred. No. 5.3e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 117; DB 14;
Pred. No. 1.2e-06;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                        1 QVWSLWALGWRWLRRYGWNM 20
                                                                                                                                                                                                                                                                                                                                     1 OVWSLWALGWRWLRRYGWNM 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.7%;
Best Local Similarity 90.0%;
Matches 18; Conservative
                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                          20; Conservative
                                                                                                                                                                                                                 Sest Local Similarity
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                                                                                                                              ; OTHER INFORM
US-10-066-965A-7
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LENGTH: 20
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Publication No. US20030143626A1
GENERAL INFORMATION:
APPLICANT: COLAS, PIERRE
APPLICANT: COHEN, BARAK A.
TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: GGYP 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT PILING DATE: 2002-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BRENT, ROGER
APPLICANT: COHEN, BRAAK A.
TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: BGYP 3.0-0.15
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT APPLICATION NUMBER: 2002-12-09
SUMUMBER OF SEQ 1D NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: No. US20030113749A1 Relevant
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100.0%; Pred. No. 5.3e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 129; DB 14; Best Local Similarity 100.0%; Pred. No. 5.3e-08; Matches 20; Conservative 0; Mismatches 0;
                      NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/311001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFRAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10066965A
Publication No. US20030143626A1
GENERAL INFORMATION:
APPLICANT: COLAS, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVWSLWALGWRWLRRYGWNM 20
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 20; Conservative
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US-10-066-965A-1
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LENGTH: 20
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APPLICANT: Frye, Catherine
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Essential for Plant Growt
TITLE OF INVENTION: Development and Uses Thereof
FILE REFERENCE: 70166USNP
CURRENT APPLICATION NUMBER: US/10/696,616
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                                                                                                          Length 2115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods for Improving Seed and Grain TITLE OF INVENTION: Methods for Improving Seed and Grain TITLE OF INVENTION: Characteristics
FILE REFERENCE: 1390
CURRENT APPLICATION NUMBER: US/10/208,948
CURRENT FILING DATE: 2002-07-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-10-25
NUMBER OF SEQ IN DNOS: 28
NUMBER OF SEQ IO NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                 6; Indels
                                                                                                        Score 60; DB 14;
Pred. No. 1.2e+02;
                                                                                                                                                   Mismatches
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Publication No. US20030074689A1
GENERAL INFORMATION:
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Olsen, Odd-Arne
APPLICANT: Shen, BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lid, Stein E.
Li, Changjiang
Jung, Rudolf
Gruis, Darren B.
Lorentzen, Jennifer A.
Ananiev, Evgueni
Nichols, Scott E.
                                                                                                        46.5%;
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ORGANISM: Arabidopsis thaliana
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McElver, John
Aux, George
Budziszewski, Greg
                                                                                                                                                                                         3 WSLWALGWRWLRRYGW 18
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Patton, David
Frye, Catherine
                                                                                                                                                   9; Conservative
                         TYPE: PRT
ORGANISM: arabidopsis
                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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                                                                US-10-208-948-4
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: II, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 2003-05-14
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF ESQ ID NOS: 204966
SEQ ID NO 187950
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APPLICANT: Corentzen, Jennifer A.
APPLICANT: Lorentzen, Jennifer A.
APPLICANT: Ananiev, Evgueni
APPLICANT: Nichols, Scott E.
APPLICANT: Nichols, Scott E.
APPLICANT: Wang, Cunxi
TITLE OF INVENTION: Methods for Improving Seed and Grain
TITLE OF INVENTION: Characteristics
FILE REFERENCE: 1390
CURRENT APPLICATION NUMBER: US/10/208,948
FILE REPERENCE: 2002-07-30
PRIOR APPLICATION NUMBER: 60/339,719
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 2115
                                            Indels
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US-10-437-963-187850
90.0%; Pred. No. 1.2e-06;
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Olsen, Odd-Arne
APPLICANT: Shen, Bo
APPLICANT: Lid, Stein E.
APPLICANT: Lid, Stein E.
APPLICANT: Lid, Changjiang
APPLICANT: Unig, Rudolf
APPLICANT: Gruis, Darren B.
APPLICANT: Lorentzen, Jennifer A.
APPLICANT: Ananiev, Evgueni
APPLICANT: Michols, Scott E.
                                                                              1 QVWSLWALGWRWLRRYGWNM 20
                                                                                                            1 QVWSSWALGWRWLRRYGWGM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10208948 Publication No. US20030074689A1 GENERAL INFORMATION:
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                                        18; Conservative
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ORGANISM: Oryza sativa
                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 9; Conserv
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                                          Matches
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; LOCATION: (70); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-860-479
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Publication No. US2030077704A1

GRERRAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PCO08C1.

CURRENT RILING DATE: 2002-02-14

PRIOR PPLICATION NUMBER: 09/764,860

PRIOR PPLICATION NUMBER: 09/764,860

PRIOR PPLICATION NUMBER: 09/764,860

PRIOR PPLICATION NUMBER: 00/10-17

PRIOR PPLICATION NUMBER: 60/179,065

PRIOR APPLICATION NUMBER: 60/114,886

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR APPLICATION NUMBER: 60/214,487

PRIOR PLING DATE: 2000-00-34

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR PLING DATE: 2000-00-14

PRIOR PLING DATE: 2000-07-16

PRIOR PLING DATE: 2000-07-16

PRIOR APPLICATION NUMBER: 60/225,447

PRIOR PLING DATE: 2000-07-16

PRIOR PLING DATE: 2000-07-16

PRIOR PLING DATE: 2000-07-16

PRIOR PLING DATE: 2000-07-16

PRIOR PLING DATE: 2000-07-14

PRIOR PLING DATE: 2000-07-14

PRIOR PLING DATE: 2000-07-14

PRIOR PLING DATE: 2000-08-14

PRIOR PLING DATE: 2000-08-14

PRIOR PLING DATE: 2000-08-14

PRIOR PLING DATE: 2000-08-14
                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERRICE: PC008
FULE REFERRICE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER: OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 479
LENGTH: 73
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Pred. No. 11;
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Best Local Similarity 47.1%;
Matches 8; Conservative
                                29 WVLWAVNWRPWRLYSW 44
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
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NAME/KEY: SITE
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US-10-074-095-479
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LOCATION: (516)..(516)
OTHER INFORMATION: The 'Xaa' at location 516 stands for Glu, Ala, Gln, or Pro.
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                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (105)...(105) OTHER INFORMATION: The 'Xaa' at location 105 stands for Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KER: misc feature
LOCATION: (553). (553)
OTHER INFORMATION: The 'Xaa' at location 553 stands for Leu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.5%; Score 60; DB 17; Length 21 Best Local Similarity 56.2%; Pred. No. 1.2e+02; Matches 9; Conservative 1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/208,948
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: 60/309,719
PRIOR FILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
| IOCATION: (1659)...(1659)
| OTHER INFORMATION: Xaa= any amino acid
US-10-696-616-16
CURRENT FILING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: US 60/423,519
PRIOR FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 16
LENGTH: 2157
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APPLICANT: Olsen, Odd-Arne
APPLICANT: Shen, Bo
APPLICANT: Lid, Stein E.
APPLICANT: Lid, Changliang
APPLICANT: Lid, Changliang
APPLICANT: Gruis, Darren B.
APPLICANT: Gruis, Darren B.
APPLICANT: Lorentzen, Jennifer A.
APPLICANT: Ananiev, Evgueni
APPLICANT: Nichols, Scott E.
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Publication No. US20030074689A1
GENERAL INFORMATION:
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 1390
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; ORGANISM: zea mays
US-10-208-948-24
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22 0/216,647 07 07 0/225,267 0/216,880 07 07 14 0/25,270 0/225,270 0/235,834 27 27 27	000000000000000000000000000000000000000	000000000000000000
. 2000-08-2 NUMBER: 66 . 2000-07-6 . 2000-07-6 . 2000-07-6 . 1 200 - 07-6 . 2000-08-1 . 2000-08-1 . 2000-08-1 . 2000-08-1 . 2000-08-1 . 2000-08-1 . 2000-08-1 . 2000-08-1 . 2000-08-1 . 2000-08-1 . 2000-09-2	UMBER: 6 2000-09-1 UMBER: 6 2000-08-1 UMBER: 6 2000-09-1 UMBER: 6 2000-010-1 UMBER: 6 2000-10-1 UMBER: 6 2000-11-1 UMBER: 6 2000-12-1 UMBER: 6 2000-09-1 UMBER: 6 2000-09-1 UMBER: 6 2000-09-1	NUMBER: 2000-0 2000-0 NUMBER: 2000-0 2000-0 NUMBER: 2000-1 NUMBER: 2000-1 NUMBER: 2000-1 NUMBER: 2000-0 NUMBER: 2000-0 NUMBER: 2000-0 NUMBER:
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OR APPLICATION UNDBER: 60/249, 215
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249, 264
OR FILING DATE: 2000-11-17
OR RELING DATE: 2000-11-17
OR FILING DATE: 2000-11-17
OR FILING DATE: 2000-11-17
OR PILING DATE: 2000-10-14 REFLICATION NUMBER: 60/235,836
RELING DATE: 2000-09-14
RAPPLICATION NUMBER: 60/235,836
RELING DATE: 2000-09-06
REPLING DATE: 2000-09-06
REPLING DATE: 2000-09-06
REPLING DATE: 2000-09-06
REPLING DATE: 2000-06-30
REPLING DATE: 2000-06-14
REPLING DATE: 2000-06-14
REPLING DATE: 2000-08-14
REPLING DATE: 2000-08-14
REPLING DATE: 2000-11-17
REPLING DATE: 2000-11-17
REPLING DATE: 2000-11-17
REPLING DATE: 2000-11-17
REPLING DATE: 2000-11-17 RAPPLICATION NUMBER: 60/249,213
RAPLICATION NUMBER: 60/249,212
RAPLICATION NUMBER: 60/249,212
RETLING DATE: 2000-11-17
RAPPLICATION NUMBER: 60/249,207
RAPLICATION NUMBER: 60/249,245
RAPLICATION NUMBER: 60/249,245
RAPLICATION NUMBER: 60/249,244
RAPLICATION NUMBER: 60/249,244
RAPLICATION NUMBER: 60/249,244
RAPLICATION NUMBER: 60/249,244 APPLICATION NUMBER: 60/232,081 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/232,080 APPLICATION NUMBER: 60/249,217 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,211 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/231,242 FILING DATE: 2000-09-08 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/231,414 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/231,244 APPLICATION NUMBER: 60/240,960 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/239,935 APPLICATION NUMBER: 60/239,937 FILING DATE: 2000-10-13 APPLICATION NUMBER: 60/241,787 FILING DATE: 2000-10-20 FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/249,216
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,210 APPLICATION NUMBER: 60/225,759 FILING DATE: 2000-08-14 LING DATE: 2000-08-14
PPLICATION NUMBER: 60/227,182 APPLICATION NUMBER: 60/246,474 FILING DATE: 2000-11-08 APPLICATION NUMBER: 60/246,532 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/226,681 APPLICATION NUMBER: 60/225,213 APPLICATION NUMBER: 60/225,214 2000-08-14 2000-10-13 2000-08-22 2000-08-22 APPLICATION NUMBER: FILING DATE: 2000-10 FILING DATE: FILING DATE: FILING DATE: PRIOR

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GENERAL INFORMATION:
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1 LOCATION: (70)

2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-212-872-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (30) TOTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 479, Application US/10212872; Publication Vo. US20030215893A1; Publication No. US20030215893A1; GENERAL INFORMATION:

APPLICANT: Rosen et al.; APPLICANT: Rosen et al.; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFRENCE: PC008C2 LORS.

CURRENT APPLICATION NUMBER: US/10/212,872; CURRENT FILING DATE: 2002-08-07; Prior application removed - See File Wrapper or Palm, NUMBER OF SEQ ID NOS: 1198; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 479; LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.7%; Score 59; DB 14; Length 73; Best Local Similarity 47.1%; Pred. No. 11; Matches 8; Conservative 3; Mismatches 6; Indels
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; Publication No. US20040031072A1
                                         PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/23,063
PRIOR APPLICATION NUMBER: 60/23,063
PRIOR PLING DATE: 2000-09-14
PRIOR PLING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR PLING DATE: 2000-09-14
PRIOR PELING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,21
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
                          60/233,064
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16 IWSMWLPGEQWLRPXSW 32
FILING DATE: 2000-09-08
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
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APPLICANT: LA KOVALICA,

APPLICANT: LA KOVALICA,

APPLICANT: Expu, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bribarla, Flad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221) B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 187848

LENGTH: 2160
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21 (53223) B
TURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/203-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
45.7%; Score 59; DB 15; Length 135;
Best Local Similarity 53.3%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_105784C.1.pep
US-10-424-599-149236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Clone ID: PAT_MRT4530_84510C.1.pep. US-10-437-963-187848
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 187848, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 WRKWGCGWRWGARWG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WSLWALGWRWLRRYGW 18
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Best Local Similarity 50.v.
The Book Conservative
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                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-437-963-187848
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 26, 2004, 06:19:49 ; Search time 17 Seconds (without alignments) 113.196 Million cell updates/sec Run on:

US-10-066-965A-2 129 1 QVWSSWALGWRWLRRYGWGM 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable alkane by	- ro		Burface a	surface	surface	surface	surface	μ			type IV prepilin p		hypothetical prote	u			O)	hypothetical prote	major surface anti	2	surface antigen -	small surface prot	surface antigen -			U,	surface r	conserved hypothet
SUMMARIES	ID	B83454	148192	SAVL64	SAVLC	SAVLS	SAVL59	SAVL7	SAVLW8	G96595	F72226	T04772	C53374	F72335	S74708	W4BP77	D75078	C83311	SAVLC2	B83755	JQ1579	JQ1580	JQ2119	JQ2225	JQ2122	J02121	J02120	J02226	JQ2230	A83325
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۵	Query Match	44.2	42.6	42.6	42.6	42.6	42.6	42.6	42.6	•	41.1	41.1	40.3	•	ö	6	6	39.5	39.5	39.5	œ.	38.8	38.8		œ.				о О	38.4
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conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote	probable acetyltra	acetyltransferase	conserved hypothet	hypothetical prote	probable muramoy1-	hypothetical prote	O-acetylserine syn	conserved hypothet	hypothetical 30.0K	probable permease	phage protein homo	TOTAL CO TYPE TOTAL
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389	425	16	m	1.,											
	37.6 425				36.8	36.8	36.8	36.8	36.4	36.4	36.4	36.4	36.4	36.4	36 4
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ALIGNMENTS

2;

Gaps

4;

Ouery Match 42.6%; Score 55; DB 2; Length 123; Best Local Similarity 57.9%; Pred. No. 3.1; Matches 11; Conservative 1; Mismatches 3; Indels

<DSA>

5

Gaps

4;

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C;Species: ground squirrel hepatitis virus
C;Accession: A03709
R;Secies. C; Ganem, D; Varmus, H.E.
J. Virol. 51, 367-375, 1984
A;Title: Nucleotide sequence of an infectious molecularly cloned genome of ground squirr
A;Accession: A03709
A;Accession: A03709
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A;Accession: A03709
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A;Accession: A
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N;Contains: major surface antigen; middle surface antigen
C;Species: woodchuck hepatitis virus
C;Daccession: H29969
E;Cohen; J.I.; Miller, R.H.; Rosenblum, B.; Denniston, K.; Gerin, J.L.; Purcell, R.H.
Virology 162, 12-20, 1988
A;Title: Sequence comparison of woodchuck hepatitis virus replicative forms shows conser
A;Reference number: A94368; MUID:88101359; PMID:3336938
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A,Cross-references: UNIPROT:P12910, GB:M19183; NID:g336141; PIDN:AAA46762.1; PID:g336142
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N;Contains: major surface antigen; middle surface antigen
C;Species: woodchuck hepatitis virus
C;Species: woodchuck hepatitis virus
C;Accession: D2969
R;Cohen, JI.; Miller, R.H.; Rosenblum, B.; Denniston, K.; Gerin, J.L.; Purcell, R.H.
Virology 162, 12-20, 1988
A;Titler: Sequence comparison of woodchuck hepatitis virus replicative forms shows conser A;Reference number: A94368; MUID:88101359; PMID:3336938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: glycoprotein; surface antigen (gene pre-S2/S) #status predicted F;147-428/Product: middle surface antigen (gene S) #status predicted <MSA-728/Product: major surface antigen (gene S) #status predicted <MSA-F;149/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 10;
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N; Contains: major surface antigen; middle surface antigen
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Pred. No. 10;
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C,Superfamily: hepatitis B virus surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: UNIPROT: P03144; GB: K02715 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSWALGSYLWEWALARFSW 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 SSWALGNYLWEWALARFSW 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SSWALG---WRW-LRRYGW 18
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Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
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Best Local Similarity
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A; Gene: pre-S1/pre-S2/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                     Accession: 1282 Acres on tigen precursor - woodchuck hepatitis virus (clone 64)

Middle surface antigen precursor - woodchuck hepatitis virus (clone 64)

N; Contains: major surface antigen
C; Species: woodchuck hepatitis virus
C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C; Accession: 128948

R; Etiemble, J.; Moercey, T.; Trepo, C.; Tiollais, P.; Buendia, M.A.
Gene 50, 207-214, 1986
A; Title: Nucleocitde sequence of the woodchuck hepatitis virus surface antigen mRNAs and
A; Reference number: A91568; MUID:87219879; PMID:3582979
A; Accession: B29498
A; Moter number: A91568; MUID:87219879; PMID:3582979
A; Moter number: A91568; MUID:8719879; PMID:3582979
A; Coss-references: UNIPROT:P11293; GB:MIS954; NID:g093289; PIDN:AAA69574.1; PID:g336156
C; Generics:
A; Gene: pre-S2/S
C; Superfamily: hepatitis B virus surface antigen
C; Keywords: glycoprotein; signal sequence #status predicted cS1G>
F; A; Binding site: carbohydrate (Asn) (covalent) #status predicted
F; A; Binding site: carbohydrate (Asn) (covalent) #status predicted
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R.Galibert, F.; Chen, T.N.; Mandart, E.
J. Virol. 41, 51-65, 1982
J. Virol. 403707
J. Virol. 
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N;Contains: major surface antigen; middle surface antigen
C;Species: woodchuck hepatitis virus
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 42.6%; Score 55; DB 1; Length 282; Best Local Similarity 57.9%; Pred. No. 6.9; Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                          SSWALGNYLWEWALARFSW 69
                                                                    SSWALG ---WRW-LRRYGW
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Best Local Similarity 57.9%;
Matches 11; Conservative
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R,Galibert, F.; Chen
J. Virol. 41, 51-65,
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à g Gaps

RESULT 5 SAVLS

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359

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RESULT 8 SAVLWB

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A;Cross-references: UNIPROT:Q9X208; GB:AE001808; GB:AE000512; NID:g4982233; PIDN:AAD3674; A;Experimental source: strain MSB8 C;Genetics:
   A,Cross-references: UNIPROT:Q9C8A6; GB:AE005173; NID:g10645420; PIDN:AAG21537.1; GSPDB:GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: F72226
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Accession: T04772
R.Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999
A;Reference number: 215384
A;Accession: T04772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A,Reference number: A72200; MUD:99287316; PMID:10360571
A,Accession: F7226
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-67 <ARN>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Species: Thermotoga maritima
C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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C;Superfamily: Arabidopsis thaliana hypothetical protein F10M10.30
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A;Introns: 91/1; 139/3; 416/1; 475/3; 528/3; 603/3; 683/1; 748/2
                                                                                                                                                   Length 2143;
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A;Cross-references: UNIPROT:095YZ1; EMBL:AL035521
A;Experimental source: cultivar Columbia; BAC clone F10M10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - Thermotoga maritima (strain MSB8)
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41.2%; Pred. No. 35;
tive 3; Mismatches 7;
                                                                                                                                                      2;
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                                                                                                                                                Score 54; DB 2
Pred. No. 64;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                   41.9%;
50.0%;
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                                                                                                                                                                                                                                                                                                                               28 WILWAVNWRPWRLYSW
                                                                                                                                                Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity
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                              C,Genetics:
A,Gene: F7A10.23
A,Map position: 1
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Keference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G96595
A)Residues: 1-431 <COH>
A;Cross-references: UNIPROT:P12909; GB:M18752; NID:G336136; PIDN:AAA46766.1; PID:G336137
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: B32397
R,Girones, R.; Cote, P.J.; Hornbuckle, W.E.; Tennant, B.C.; Gerin, J.L.; Purcell, R.H.; Proc. Natl. Acad. Sci. U.S.A. 86, 1846-1849, 1989
A;Title: Complete nucleotide sequence of a molecular clone of woodchuck hepatitis virus A;Reference number: A34222; MUID:89184524; PMID:2928306
A;Accession: B32397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;150-431/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F;210-431/Product: midor surface antigen (gene S) #status predicted <MSA>
F;32,94,152/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                 A.Gene: pre-S1/pre-S2/S
C.Superfamily: hepatitis B virus surface antigen
C.Superfamily: hepatitis B virus surface antigen
C.Supervoluct: middle surface antigen
F.150-431/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F.210-431/Product: major surface antigen (gene S) #status predicted <MSA>
F.32,94,152/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        large surface antigen - woodchuck hepatitis virus (clone 8)
N;Contains: major surface antigen; middle surface antigen
C;Species: woodchuck hepatitis virus
C;Species: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F7A10.23 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: G96595
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                            42.6%; Score 55; DB 1; Length 431; 57.9%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.6%; Score 55; DB 1; Length 431; larity 57.9%; Pred. No. 10; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P17400; GB:J04514
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SSWALG---WRW-LRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
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Best Local Similarity
Matches 11; Conserva'
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-431 <GIR>
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Query Match Best Loca Matches

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Search completed: October 26, 2004, 06:46:22 Job time : 17 secs
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene 4.7 protein - phage T7
C;Species: phage T7
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A; Residues: 1-135 < DUN>
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A; Residues: 1-135 < DUW>
A;Status: preliminary
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                                                             type IV prepilin peptidase (EC 3.4.99.-) pilD - Neisseria lactamica (strain LNP411) (fra N.Contains: type IV pilin N-methyltransferase (EC 2.1.1.-) c.Species: Neisseria lactamica c.hate: 23-Mar-1995 #text_change 29-Jan-1999 c.hate: 23-Mar-1995 #text_change 29-Jan-1999 c.hate: 23-Mar-1995 #text_change 29-Jan-1999 c.hate: 23-Mar-1995 #text_change 29-Jan-1999 c.hatesion: C53374 #sequence_revision 23-Mar-1995 #text_change 29-Jan-1999 c.hately Dupuy, B. Pupuy, B. Pupuy, B. Pupuy, B. Pupuy, A.P. Pupuy, B. Pupuy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein TM0760 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72335
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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Affille: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72335
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A;Experimental source: strain MSB8
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C;Accession: S74708
R;Kancko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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Mypothetical protein slr1306 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.3%; Score 52; DB 2; Length 102; 54.5%; Pred. No. 6.2;
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: pilD
C;Superfamily: type IV prepilin peptidase
C;Keywords: hydrolase; methyltransferase; S-adenosylmethionine
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ilarity 61.5%;
Conservative
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113 SWSLGWYYVRRKG 125
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Best Local Similarity
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A, Residues: 1-102 <DUP>
C, Genetics:
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A,Molecule type: DNA A.Residues: 1-485 - KZNA.
A,Kesidues: 1-485 - KZNA.
A,Cross-references: UNIRROT:P72844; EMBL:D90901; GB:AB001339; NID:91651897; PIDN:BAA16855
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT: P03786
R;Dun, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A;Title: Complete mucleotide sequence of bacteriophage T7 DNA and the locations of T7 ger A;Reference number: $42283; MUID: 83241725; PMID: 6864790
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40.3%; Score 52; DB 2; Length 485;
Best Local Similarity 45.0%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 34.87-35.88
C;Superfamily: phage T7 gene 4.7 protein
                                                                                                                                                                                                                                                        3 WSSWALG-----WRWLRRY 16
                                                                                                                                                                                                                                                                                                            45 WGLWALSGLGLVIWRWRRRH 64
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OrderedLoousNames=MAP2949c;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteriues;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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les 8; Conserv
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6.1444
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(without alignments)
123.736 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2: uniprot_trembl:*
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Bad07761 oryza sat
Q9x208 thermotoga
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Q73tc3 mycobacteri
Aas06345 mycobacte
Q6ih30 drosophila
                      Q9c8a6 arabidopsis
                                    Q8rvl2 arabidopsis
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 Q94e52
P70570
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Akopiants K.E., Danilenko V.N.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akopiants K.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 AA; 28490 MW; D2AD3F681470264E CRC64;
                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Manincylycoside-O-phosphotransferase type 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01636; APH; 1. PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%; Score 63; DB 2; 50.0%; Pred. No. 2.8;
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                                                                                                                                                                                                          ALIGNMENTS
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GO; GO:0016740; F:transferase activity;
InterPro; IPR002575; APH trans.
InterPro; IPR011009; Kinase_like.
InterPro; IPR00256; Tyr_pkinase_AS.
Pfam; PF01636; APH; I
                                                                                                                            Q73TC3
AAS06345
Q6IH30
                                                                        Q6ZFZ4
BAD07761
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                                   QBRVL2
QBRUQ1
QBRVL1
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            P70570
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                       Ryan R.P., Ryan D.J., Dowling D.N.; "The Xme-like system of strain Xanthomonas campestris IG8 mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellula
                              13;
                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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Length 488;
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                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    metal resistance.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY359472; AAT39386.1; -.
Hypothetical protein.
SEQUENCE 4188 AA; 52189 MW; 8B16A7998475E512 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL. BX294136; CAD72307.1; -.
COMplete proteome; Hypothetical protein.
SEQUENCE 466 AA; 53606 MW; F6FFC58A6FD97A97 CRC64;
                                                                                                                                                                                                  01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Score 60.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.0%; Score 58; DB 2;
64.3%; Pred. No. 21;
tive 1; Mismatches
                                                                                                                                                                      488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.9%; Score 60.5; C 41.4%; Pred. No. 11; ative 1; Mismatches
                Pred. No. 11;
1; Mismatches
                                                                                VWGSWLLASAPLFVIFNALGW-WLDAFGW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 VWGSWLLASAPLFVIFNALGW-WLDAFGW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- ALGWRWLRRYGW 18
                                                           2 VWSSW------ALGWRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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46.98;
              ilarity 41.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41.4'
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=RB1870;
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                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                  campestris
                                                                                                                                                                                                                                               Hypothetical protein
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            Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                  Kanthomonas
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 Query Match
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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EMBL; AE01737; AAS05266.1; -.
Hypothetical protein.
SEQUENCE 312 AA; 35001 MW; 577E4AE35A177103 CRC64;
                                          Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017237, AAS05266.1; -
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                   Query Match 47.3%; Score 61; DB 2; Length 312; Best Local Similarity 50.0%; Pred. No. 6; Matches 8; Conservative 4; Mismatches 4; Indels
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6;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, 34359472; ART39386.1; -.
Hypothetical protein Protein SEQUENCE 488 AA, 52189 WW, 8B16A7998475E512 CRC64;
                                                                                                                                    Complete proteome, Hypothetical protein.
SEQUENCE 312 AA; 35001 MW; 577E4AE35A177103 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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NCBI_TaxID=1770;
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                SEQUENCE FROM N.A.
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AAS05266;
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Query Match
Best Local Similarity
Matches 10; Conserv
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Name=alkB2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUB=Bone;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Than Palysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=20499314; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                        01-MRN-2003 (TIENBLIFE): 23, Last sequence update)
01-MRN-2003 (TIENBLIFE): 23, Last annotation update)
Mus musculus adult male bone CDNA, RIKEN full-length enriched library,
clone: 9830169C09 product:ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-TRNA LIGASE) (ALARS) homolog.
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STRAIN=C57BH/6J; TISSUE=Bone;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Hayatsu N., Hishi Y., Itoh M., Kagawa I., Kaswa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kowda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57EL/6J; TISSUE=Bone;
MEDLINE=20530913; PubMed=11076861;
Shibatea K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibatea K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Fujiwake S., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-334-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Bone; MEDILMB=21.08560; PubMed=11217851; RIKBN FANTOM CORSOLIUM; COROSOLIUM; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=99279253; PubMed=10349636;
Carninoi, P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                             164 AA.
                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meth. Enzymol. 303:19-44(1999)
               197 ÇAWSÇWSLSKRWLR 210
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                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    (Mouse)
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
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Q8BZ40;
                                                                                          RESULT 7
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Ή, ·, Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takakusahi F., Takakus A., Takakus Y., Tanaka T., Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Gaps Gaps MEDLINE=22225697; PubMed=12917641; DOI=10.1038/nature01943; Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L., Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J., Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.; "The genome of a motile marine Synechococcus."; Mature 424:1037-11642(2003).

BMBL: BX569689; CAE06731.1; COO GO: 0003948; F:2-anino-4-hydroxy-6-hydroxymethyldihydropte. GO; GO: 0016740; F:transferase activity; IEA.
GO; GO: 000396; P:folic acid and derivative biosynthesis; IEA. InterPro; IPR000276; GPCR. Rhodpsn. 1; 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative alkane-1-hydroxylase (Putative alkane-1-monooxygenase) ; Length 164; Length 163; Indels Indels D73DC68F0E60F610 CRC64; 163 AA; 17774 MW; 39D2021EA256F92F CRC64; Synechococcus sp. (strain WH8102)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus. NCBL_TaxID=84588; GO; GO:0004813; F:alanine-tRNA ligase activity; IEA. GO; GO:0016874; F:ligase activity; IEA. Aminoacyl-tRNA synthetase; Ligase. SEQUENCE 164 AA; 18827 MW; D73DC68F0E60F610 CRC6 Pfam, PF01288; HPPK; 1.
TIGRPAMS; TIGROL488; FOLK; 1.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00794; HPPK; 1. DB 2; 44.2%; Score 57; DB 2; 83.3%; Pred. No. 10; iive 1; Mismatches 44.6%; Score 57.5; DB 58.8%; Pred. No. 9.1; Live 2; Mismatches 163 AA 241 AA Complete proteome; Kinase; Transferase pyrophosphokinase (EC 2.7.6.3).
Name=folK; OrderedLocusNames=SYNW0216; PRT; PRT; 18 91 3 WSSWAL-GWRWLRRYGW 75 WTFWALAGFRWLPGMGW Conservative 10; Conservative 1 QVWSSWALGWRW 12 42 OVWSSOALGFRW 53 PRELIMINARY; PRELIMINARY;

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Pseudomonas aeruginosa
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Morales G., Wiehlmann L., Gudowius P., van Delden C., Tummler B.,
Martinez J., Rojo F.;
"Structure of Pseudomonas aeruginosa Populations Analyzed by Single
Nucleotide Polymorphism and Pulsed-Field Gel Electrophoresis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                     Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
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                                                                                        SEQUENCE FROM N.A.
Belhaj A., Desnoues N., Elmerich C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ344081; CAC86946.1; -.
EMBL; AJ344085; CAC86949.1; -.
EMBL; AJ344088; Fanconoxygenase activity; IEA.
InterPro; IFR005804; Fa desat.
Pfam; PF00487; FA_desaturase; 1.
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EMBL; AJG33616; CAG17608.1; -.

InterPro; IPROOS804; Fa desat.

Fram; PF00487; FA desaturase; 1.

SEQUENCE 377 AA; 43386 MW; 14D7FBF9D6714E2E CRC64;
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27244 MW; 50028AF229AB196C CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alkane hydroxylase.
Name-alkB2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 VWSGWILAHETRWDWVGQLGW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VWSSWALG----WRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VWSSWALG----WRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 VWSGWILAHETRWDWVGOLGW 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               os-oul-2004 (TrEMBLrel. 27, C. 05-JUL-2004 (TrEMBLrel. 27, La 05-JUL-2004 (TrEMBLrel. 27, La Alkane hydroxylase.
                                       Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                          44.2%;
                                                                                                                                                                                                                                                                                                                                                                         Similarity 42.9
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 42.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                     241 2
241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=287;
                                                         NCBI_TaxID=287;
                                                                                                                                                                                                                                                                   Monooxygenase.
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NON TER
SEQUENCE
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Best Local S
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Q6H936
ID Q6H93
AC Q6H93
DT 05-JU
DT 05-JU
DT 05-JU
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,GN Name=
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Gaps
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STRAIN=RRI, FG. 1892, G7, DM, HJ2, 63741, SG31, ATCC10145,
STRAIN=RRI, K9, SG1, 892, G7, DM, HJ2, 63741, SG31, ATCC15524, and
ATCC15691, ATCC33356, ATCC33818, 19G12, CECT119, ATCC15524, and CHA;
Morales G., Wiehlmann L., Gudowius P., van Delden C., Tummler B.,
Martinez G., Rojo F.;
"Structure of Pseudomenas aeruginosa Populations Analyzed by Single Nucleotide Polymorphism and Pulsed-Field Gel Electrophoresis
                                                                                                             STRAIN=DEMIL28;
Morales G., Wiehlmann L., Gudowius P., van Delden C., Tummler B.,
Martinez J., Rojo F.;
Martinez G., Rojo F.;
Martinez G. Pseudomonas aeruginosa Populations Analyzed by Single
"Structure of Pseudomonas aeruginosa Populations Analyzed by Single
Nucleotide Polymorphism and Pulsed-Field Gel Electrophoresis
Genotyping.";
G. Bacteriol. 186.4228-4237(2004).
U. Bacteriol. 186.4228-4237(2004).
U. Bacteriol. 186.4228-631;
U. Bacteriol. 186.4228-631;
F. Gesat.
Pfam: PF00487; F. Gesat.
SEQUENCE 377 AA; 43342 MW; GF7BEBA795802C9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                             44.2%; Score 57; DB 2; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pfam; PF00487; FA desaturase; 1.
SEQUENCE 377 AA; 43408 MW; 1F23438DA9F1822E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.9%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 VWSGWILAHETRWDWVGQLGW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 186:4228-4237(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VWSSWALG----WRWLRRYGW 18
                         Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ633602; CAG17594.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27, 27, 28, 1
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AJ633620; CAG17612.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAG17609.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAG17606.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAG17607.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ633604; CAG17596.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAG17610.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAG17605.1
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AJ633608; CAG17600...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ633609; CAG17601.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAG17602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAG17604.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alkane hydroxylase.
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ633617;
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                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
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9; Conservative

Matches

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Search completed: (
Job time : 93 secs
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AAR13803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
MEDLINE-2043737; Pubmed=1094043;
SCOVET C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Nu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas frederiksbergensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=104087;
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  Indels
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Abdel-Megeed A.F., Mueller R.M.;
Abdel-Megeed A.F., Mueller R.M.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; A7452488; AAR13803.1; -.
InterPro; IPR005804; Fa_desat.
Pfan, PF00487; FA_desaturase; 1.
SEQUENCE 700 AA; 77128 MW; EOBID75998E14AB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004581; AA634914.1; -.
PIR; B83454; B83454.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005804; Fa_desat.
Interpro; IPR005804; Fa_desaturase; 1.
Complete proteome; Monooxygenase.
SEQUENCE 377 AA; 43408 MW; IF23438DA9F1822E CRC64;
                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
  . 9
                                                                                                                                                                                                                                        377 AA.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Alkane-1-monooxygenase 2.
Name=alkB2; OrderedLocusNames=PA1525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                        PRT;
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                                                                                                      101 VWSGWILAHETRWDWVGQLGW 121
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                                                 2 VWSSWALG----WRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VWSSWALG----WRWLRRYGW 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
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Name=alkB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=287;
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                                                                                                                                                                                                                                     091318
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Q6SQM6
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44.2%; Score 57; DB 2; Length 700;

Query Match

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                          Gaps
                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Alkane monooxygenase gene of Pseudomonas frederiksbergensis."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AY452488; AAR13803.1; SEQUENCE 700 AA; 77128 WW; BOEID75998E14AB6 CRC64;
                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 700;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                            AAR13803;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Alkane hydroxylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 2;
Pred. No. 42;
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42.9%; Pred. No. 42,
... 2; Mismatches
                                                                                                                                                                                              700 AA
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: October 26, 2004, 06:39:20
      Pred. No.
                                                                                                                                                                                                PRT;
                                                          2 VWSSWALG----WRWLRRYGW 18
                                                                                  23 VWSGWILAHETRWDWVGQLGW 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VWSSWALG----WRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Abdel-Megeed A.F., Mueller R.M.;
                        2;
                                                                                                                                                                                                                                                                                                                              Pseudomonas frederiksbergensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 VWSGWILAHETRWDWVGQLGW
  42.98;
Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=104087;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                 OM protein - protein search, using sw model
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October 26, Run on:

2004, 06:09:56; Search time 85.5 Seconds (without alignments) 83.913 Million cell updates/sec

US-10-066-965A-2 129 1 QVWSSWALGWRWLRRYGWGM 20

Perfect score: Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
geneseqp2001s:*
geneseqp201s:*
geneseqp203as:*
geneseqp203as:* A_Geneseq_23Sep04:* 1: genesecp19R0s.* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2004s:*

SUMMARIES

		a			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
П	129	100.0	20	5	AA018008	Aao18008 Intracell
7	117	90.7	20	2	AAR89346	
е	117	90.7	20	N	AAW32121	Aaw32121 Interacti
4	117	90.7	20	٣	AAY49340	Aay49340 Cdk2 inte
Ŋ	89.5	69.4	17	2	AA018007	Aao18007 Intracell
9	59	45.7	118	4	ABG24883	Abg24883 Novel hum
7	57	44.2	382	7	AB083419	Abo83419 Pseudomon
80	57	44.2	1086	7	AB076305	Abo76305 Pseudomon
σ	26	43.4	73	4	AAU17861	Aaul7861 Novel hum
10	26	43.4	73	7	ADG41241	Adg41241 Human res
11	26	43.4	122	ω	ADG22291	Adg22291 Cyanophag
12	55.5	43.0	78	8	ADG22339	Adg22339 Cyanophag
13	55.5	43.0	136	9	ABR56763	
14	52	42.6	282	N	AAY32836	Aay32836 Woodchuck
15	54.5	42.2	452	Ŋ	ABB92178	Abb92178 Herbicida
16	54.5	42.2	574	9	ABJ39104	Abj39104 Molecule
17		41.9	69	4	AAM80357	Aam80357 Human hae
18	54	41.9	599	4	ABG18132	Abg18132 Novel hum
19	5. 4.	41.9	1725	٣	AAB48460	Aab48460 Rat lamin
20	54	41.9	2115	φ	ABP70920	Abp70920 Arabidops
21	54	41.9	2150	φ	ABP70925	
22	54	41.9	2159	9	ABP70924	Abp70924 Maize DEK
23	53	41,1	89	4	ABG06199	Abg06199 Novel hum
24	53	41.1	105	4	ABG11452	Novel
25	52.5	40.7	173	7	AB083613	Pseudo

Aau57671 Propionib	Abm54190 Propionib	Abo58643 Human gen	Abo62629 Klebsiell	Aaul6958 Human nov	Abb10301 Human cDN	Abp66888 Human pol	Abu22728 Protein e	Aaw09046 WHV core-	Abo82724 Pseudomon	Adc78292 Human mig	Aam20859 Peptide #	Abb42638 Peptide #	Aam36452 Peptide #	Abb25984 Protein #	Aam76343 Human bon	Aam63529 Human bra	Abg58051 Human liv	Abg45636 Human pep	Aab33896 Human sec
AAU57671	ABM54190	ABO58643	AB062629	AAU16958	ABB10301	ABP66888	ABU22728	AAW09046	AB082724	ADC78292	AAM20859	ABB42638	AAM36452	ABB25984	AAM76343	AAM63529	ABG58051	ABG45636	AAB33896
4	φ	ω	7	4	4	Ŋ	ø	N	7	7	4	4	4	4	4	4	4	ເກ	r
9	09	105	115	242	242	242	261	346	480	41	45	45	45	45				45	
40.3	40.3	40.3	39.9	٠.	9	39.9	-:	39.5	39.5	38.8			38.8			ω,	38.8		38.8
52	52		51.5	51.5	51.5	~	51	51	51	20	20		20					20	
56	27	28	59	30	31	32	33	34	32	36	37	38	39	40			43	44	45

ALIGNMENTS

RESU	RESULT 1
AA01	AAO18008
ID	AA018008 standard; peptide; 20 AA.
X	
AC	AA018008;
X	, , , ,
DŢ	30-AUG-2002 (first entry)
X	
DE	Intracellular target molecule property modulation method aptamer
X	
X	Intracellular target; cellular component; property modulation;
ΜX	antimicrobial; immunomodulatory; nootropic; neuroprotective; meta
X	neuroleptic; cytostatic; cardiant; infection; immunological disor
X	neurological disorder; metabolic disorder; psychiatric disorder;
Ϋ́	myopathy; cancer; cardiovascular disorder.
X	

abolic;

rder;

10M.

Unidentified.

EP1205191-A1

15-MAY-2002.

13-NOV-2000; 2000EP-00403156

13-NOV-2000; 2000EP-00403156.

(CNRS) CENT NAT RECH SCI. (MASS-) MASSACHUSETTS GEN HOSPITAL. (MOLE-) MOLECULAR SCI INST.

Cohen BA; Colas P, Brent R,

WPI; 2002-418829/45

Process for specifically modulating the properties of an intracellular target molecule used for the treatment of various disorders.

Example 1; Fig 1; 33pp; English.

The present invention relates to a process for specifically modulating the properties of an intracellular target molecule T, and/or of a cellular component C which interacts directly or indirectly in a cell with the target. The process involves the introduction into the cell of a chimeric molecule known as a targeted effector, comprising a recognition moiety capable of recognising T and an effector moiety. The chimeric protein or nucleic acid can be used in the preparation of a medicament for the treatment of microbial infections, immunological disorders, neurological disorders, psychiatric disorders,

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(first entry)

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1 QVWSLWALGWRWLRRYGWNM 20

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Protein interaction; interaction trap; fusion protein; mimetic; therapeutic; detection; reporter gene.
                                                                                                                                                                                                          Interaction trap system aptamer 7.
                                                                                                     AAW32121 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMO ) GEN HOSPITAL CORP. (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-512733/47.
                                                                                                                                                                                                                                                                                                                              WO9738127-A1.
                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1996;
                                                                                                                                                                                                                                                                                                                                                              16-OCT-1997.
                                                                                                                                                                        22-APR-1998
                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                       AAW32121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brent R,
                                                                     RESULT 3
                                                                                       AAW32121
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                                                                                                                                       ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR89340-R89351 are Cdk-2 interacting peptides identified by an interaction trap assay using conformationally-constrained proteins. The assay comprises providing a host cell (esp. a yeast cell) which contains: (i) a reporter gene operably linked to a DNA-binding protein recognition site, pref. LexA; (ii) a 1st fusion gene expressing Cdk-2 covalently a conformationally-constrained (pref. with thioredoxin) protein (either expected to interact with Cdk-2 or a random peptide) covalently bonded to a gene-activating moiety, and measuring expression of the reporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as a measure of interaction between Cdk2 and the conformationally constrained protein. The same system may be applied to find proteins that interact with any other protein of interest (e.g. Ras) or proteins having
myopathies, genetic disorders, cancer, cardiovascular disorders and dental disorders. The present sequence is a mutant of a known anti-Cdk2 aptamer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interaction trap systems using conformationally-constrained proteins useful for detection of protein interactions and for identification and isolation of interacting proteins.
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Cdk2; cyclin dependent kinase 2; assay; identifying; isolating; cell cycle; interaction; antagonist; conformationally-constrained; agonist; interaction trap; thioredoxin; LexA; two-hybrid system.
                                                                                                                                                                                                                                                                                                                                                                                                  Cdk2-interacting peptide isolated using interaction trap assay.
                                                                                                                                       ·;
                                                                                                       Length 20;
                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agonist or antagonist activity on such interactions
                                                                                                    Score 129; DB 5;
Pred. No. 8.7e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu C;
                                                                                                                                                                                                                                                                                               A.
                                                                                                                                                                                               OVWSSWALGWRWLRRYGWGM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 66; Page 60; 73pp; English.
                                                                                                                                                                         1 OVWSSWALGWRWLRRYGWGM 20
                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jessen TH,
                                                                                                                                                                                                                                                                                              AAR89346 standard; peptide; 20
                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US009307.
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP.
                                                                                                                    1 Similarity 100.
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mccoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-105852/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 AA;
                                                                     Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9602561-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                10-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brent R,
                                                                                                                                                                                                                                                                                                                              AAR89346;
                                                                                                     Query Match
Best Local S
                                                                                                                                       Matches
                                                                                                                                                                                                                                                            RESULT 2
                                                                                                                                                                                                                                                                            AAR89346
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Jessen TH,

Mccoy JM,

97WO-US005793. 96US-00630052.

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New trap system for detecting protein interactions - comprises a reporter gene linked to a DNA-binding-protein recognition site and fusion proteins to test for interactions.
                                                                                                                                                                                                                         Aptamers AAW32116-W32132 have been isolated from a peptide library and are used in a novel interaction trap method for detecting protein interactions and isolating novel proteins. The method involves a host cell containing a reporter gene operably linked to a DNA-binding-protein (DBP) recognition site, a fusion gene capable of expressing a fusion protein which is able to specifically bind to the DBP recognition site and a second fusion gene which expresses a second fusion protein which is conformationally constrained and bonded to a gene activating molety. Measuring expression of the reporter gene gives a measure of the interaction between Pl and P2. This method can be used to identify agonists or antagonists for use as therapeutic molecules or for the design of simple molecule mimetics. The method is specifically used to detect an interacting protein in a population of proteins or to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a candidate interactor. Using conformationally constrained proteins can provide for tertiary structural analysis and can also protect proteins from cellular degradation and/or increase the protein's solubility, and/or otherwise alter the capacity of the candidate interactor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 117; DB 2; Length 20;
Pred. No. 2.9e-08;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
AAY49340
ID AAY49340 standard; peptide; 20 AA.
                                                                                                                                                         Claim 73; Page 52; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 OVWSSWALGWRWLRRYGWGM 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 AA;
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0

Gaps

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90.7%; Score 117; DB 2; Length 20; 90.0%; Pred. No. 2.9e-08; ive 0; Mismatches 2; Indels

1 OVWSSWALGWRWLRRYGWGM 20

18; Conservative

Matches

Local Similarity

Query Match

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us-10-066-965a-2.rag

13-NOV-2000; 2000EP-00403156.

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The invention relates to a population of Saccharomyces and/or mammalian cells comprising recombinant DNA molecules encoding fusion proteins, each consisting of a candidate interactor peptide, a conformation-constraining protein and a DNA binding moiety and/or gene activating moiety. The cells are useful for detecting protein interactions. The cells may also be used in a method for identifying and purifying genes encoding a wide range of useful proteins based on their physical interaction with a second
                                                                                                                                                                                                                                                                                                                                                                                                                                            Population of Saccharomyces and/or mammalian cells comprising recombinant DNA encoding fusion proteins, useful for detecting protein interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antimicrobial; immunomodulatory; nootropic; neuroprotective; metabolic; neuroleptic; cytostatic; cardiant; infection; immunological disorder; neurological disorder; metabolic disorder; psychiatric disorder; myopathy; cancer; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Intracellular target molecule property modulation method aptamer 10.
                                                                                                         Saccharomyces; mammalian; fusion protein; interactor peptide; conformation-constraining protein; DNA binding moiety; Cdk2; gene activating moiety; protein interaction; gene purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intracellular target; cellular component; property modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.7%; Score 117; DB 3; Length 20 90.0%; Pred. No. 2.9e-08; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3B; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO18007 standard; peptidė; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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                                                                                                                                                                                                                                                                                                                                                                                  Brent R;
                                                                           Cdk2 interacting peptide i5-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVWSLWALGWRWLRRYGWNM
                                                                                                                                                                                                                                                                                                   94US-00278082.
                                                                                                                                                                                                                                                                     95US-00504538
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                 GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                               GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Jessen TH,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-072059/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 AA;
                                                                                                                                                                                                                                                                    20-JUL-1995;
                                                                                                                                                                                                                                                                                                   20-JUL-1994;
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                                              14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                       US6004746-A
                                                                                                                                                                                                                                      21-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide
                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                 Mccoy JM,
                AAY49340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA018007;
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1;
                                                                                                                                                                                                                                                                                The present invention relates to a process for specifically modulating the properties of an intracellular target molecule T, and/or of a cellular component C which interacts directly or indirectly in a cell with the target. The process involves the introduction into the cell of a chimeric molecule known as a targeted effector, comprising a recognition moiety capable of recognising T and an effector moiety. The chimeric protein or nucleic acid can be used in the preparation of a medicament for the treatment of microbial infections, immunological disorders, metabolic disorders, psychiatric disorders, myopathies, genetic disorders, candiovascular disorders, and dental disorders. The present sequence is a known anti-Cdk2 aptamer used in the exemplification of the invention
                                                                                                                                                                                                          Process for specifically modulating the properties of an intracellular target molecule used for the treatment of various disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e mapping; gene mapping; gene therapy; forensic; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 89.5; DB 5;
Pred. No. 7.9e-05;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #24874.
                                                                                                     (MASS-) MASSACHUSETTS GEN HOSPITAL. (MOLE-) MOLECULAR SCI INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG24883 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVWSSWALGWRWLRRYGWGM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OVWSLWALGWRW---YGWKM 17
                                                                                                                                                                                                                                                       Example 1; Fig 1; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                           13-NOV-2000; 2000EP-00403156.
                                                                                                                                                   Cohen BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%;
Matches 15; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                       (CNRS ) CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002 (first entry)
                                                                                                                                                                            WPI; 2002-418829/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS89070.
                                                                                                                                                  Brent R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                  Colas P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG24883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
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Gaps

0;

Length 20;

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sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerlectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of stee expressing (II). (I) are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the way are appeared by the printed specification, but was obtained in the way are appeared by the printed specification of mutation and sequences.
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                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II)
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                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.7%; Score 59; DB 4; Length 118; 60.0%; Pred. No. 4.3;
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                                                                                                                                                                                                          Claim 20; SEQ ID NO 55242; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABO83419 standard; protein; 382 AA
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52 WALWSRGWRLLRRLG 66
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Best Local Similarity
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Bush D;

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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and plantage interapt of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a carterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO8486 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but, was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to Pseudomonas aeruginosa polypeptides and the polymuclectides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide,
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pathological conditions resulting from bacterial infection
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                                  Disclosure; SEQ ID NO 32165; 455pp; English
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98US-0094190P.
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for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-deruge peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences for pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this parent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                      Human, respiratory antigen, respiratory disorder, throat disorder, lung disorder, nose disorder, lung cancer, gene therapy, cytostatic, anti allergic, anti asthmatic, anti inflammatory, olfactory,
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                                                                                                                                    44.2%; Score 57; DB 7; Length 1086; 62.5%; Pred. No. 75; 2; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                   Novel human respiratory antigen #177
                                                                                                                                                                                                                                           AAU17861 standard; protein; 73 AA.
                                                                                                 segdata.uspto.gov/seguence.html
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200US-0180628P.
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Best Local Similarity 62.5
Matches 10; Conservative
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The present invention relates to the isolation of novel human respiratory antigens, and cDNA (AAS27869-AAS28159) and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders are of asthma, pleurisy, cystic fibrosis, emphysema, nos polymucleotide sequences of the respiratory tissues e.g. lung cancer. The polymucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAUT/88-AAUT/975 represent novel human respiratory antigens. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis.
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43.4%; Score 56; DB 4; Length 73;
Best Local Similarity 47.1%; Pred. No. 6.4;
Matches 8; Conservative 2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Barash SC, Ruben SM;
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17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
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17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
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05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-0256719P.
06-DEC-2000; 2000US-025149P.
08-DEC-2000; 2000US-0251868P.
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2000US-0249211P.
2000US-0249212P.
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17-NOV-2000; 2000US-0249209P.
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05-JAN-2001, 2001US-0259678P
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                                  08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
   08-NOV-2000;
   SEASON SE
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respiratory system antigen;
human respiratory system associated polynucleotide;
respiratory system disorder; throat disorder; vocal cord paralysis;
tensillitis; laryngitis; lung disorder; pneumonia; allergic disorder;
asthma; eosinophilic pneumonia; pleurisy; cystic fibrosis; emphysema;
histiocytosis; sarcoidosis; nose disorder; rhinitis; sinusitis; neoplasm;
cancer; respiratory tissue cancer; throat cancer; lung cancer;
cancer of the nose; gene therapy; chromosome identification; forensic;
human respiratory system associated protein; human.
                                                                                       antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
                                                                 Human respiratory system associated protein seq id 479.
ADG41241 standard; protein; 73 AA
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2000US-0190076P.
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                                            (first entry)
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08-NOV-2000;
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20-OCT-2000;
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26-SEP-2000;
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Novel respiratory system antigen and polynucleotides encoding the polypeptides, useful for treating diagnosing, treating or preventing tonsillitis, pneumonia, asthma and cystic fibrosis, emphysema, throat
                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 479; 236pp; English
                                                                                                                                                                                                                     Rosen CA, Ruben SM, Barash SC;
                                                                2000US-0250160P.
2000US-0250391P.
                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                      2000US-0249264P
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N-PSDB; ADG40949.
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08-DEC-2000; 2
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11-DEC-2000; 2
05-JAN-2001; 2
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17-NOV-2000;
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17-NOV-2000;
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Gaps 0; 43.4%; Score 56; DB 7; Length 73; 47.1%; Pred. No. 6.4; 7; Indels ative VWSSWALGWRWLRRYGW 18 Query Match
Best Local Similarity 47.1
Matches 8; Conservative à g

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RESULT 11 ADG22291

ADG22291 standard; protein; 122 AA.

ADG22291; AXD

The invention describes an isolated polypeptide (I) comprising an amino acid sequence that is at least 90% identical to polypeptide fragment of acid sequence that is at least 90% identical to polypeptide fragment of biological activity, polypeptide domain or epitope of PS, all-length biological activity, polypeptide domain or epitope of PS, full-length protein of PS, or variant, allelic variant or species homolog of PS. (I) concerned to a subject which involves determining (I) is also useful for diagnosing a pathological condition in a subject which involves determining the presence or absence of mutation or a subject which involves determining the presence or absence of mutation in (II) or determining the presence or amount of expression of (I) in a collogical sample and diagnosing a pathological condition based on the result. The human respiratory system associated polynucleotides, the polypeptides encoded by them, and antibodies that immunospecifically bind these polypeptides are useful in diagnosis, treatment, prevention and/or prognosis of disorders of respiratory system such as throat disorders (e.g., vocal cord paralysis, tonsilitis, and laryngitis), lung disorders (e.g., pneumonia), pleurisy, cystic fibrosis, emphysem, histiocytosis, cancers of respiratory tissues (e.g., throat cancer, lung cancer, and cancer of the nose). The polynucleotides are useful in gene therapy

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Cushing's syndrome; infection
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                              30-APR-2002; 2002FR-00005424.
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                                                            30-APR-2002; 2002FR-00005424
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J, Saurin W,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the entire genome of cyanophage S-2L, and to the protein encoded by it. Genes isolated from the genome of S-2L are useful for preparing enzymes for synthesis of D-bases (D = 2,6-diaminopurine), particularly D, dDMP and dDTP, or polynucleotides containing these bases, polymerases involved in metabolism of D-bases and deoxynucleotide analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides, can be used for detection and/or identification of S-2L, and for identifying agents that modulate synthesis of D-bases or polynucleotides containing them, and fusions of S-2L polypeptides with an antigon can be used to raise specific antibodies, useful for detecting S-2L. This sequence corresponds to one of the proteins encoded by the cyanophage S-
                                                                                                                                                                                                                                                                                                                                                                                                              genomic sequence for cyanophage S-2L, useful for identifying genes synthesis of 2,6-diaminopurine bases or polynucleotides containing
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                                                                         genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS.
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                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
(GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
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Robert C, Vico V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyanophage S-2L encoded protein #84.
                                            Cyanophage S-2L encoded protein #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG22339 standard; protein; 78 AA.
                                                                                                                                                                                                                             30-APR-2002; 2002FR-00005424.
                                                                                                                                                                                                 30-APR-2002; 2002FR-00005424.
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                       Marliere P, Kaminski PA,
Weissenbach J, Saurin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 80.0
les 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                New genomic sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GWRWCRRGGW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 GWRWLRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-045746/05,
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADG22255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyanophage S-2L.
                                                                                                       Cyanophage S-2L.
                                                                                                                                      FR2839079-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2839079-A1
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              26-FEB-2004
                                                                                                                                                                  31-OCT-2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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them.

Best Loc Matches

ò q RESULT 12 ADG22339

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The invention relates to the entire genome of cyanophage S-2L, and to the protein encoded by it. Genes isolated from the genome of S-2L are useful for preparing enzymes for synthesis of D-bases (D = 2,6-diaminopurine), particularly D, dDMP and dDTP, or polymucleotides containing these bases, polymerases involved in metabolism of D-bases and deoxynucleotide analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides, can be used for detection and/or identification of S-2L, and for identifying agents that modulate synthesis of D-bases or polymucleotides containing them, and fusions of S-2L polypeptides with an antigen can be used to raise specific antibodies, useful for detecting S-2L. This sequence corresponds to one of the proteins encoded by the cyanophage S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticonvulsant, mootropic, neuroprotective, cerebroprotective; anti-HIV, antiallergic; antinffammatory; thyromimetic; gene therapy; cancer; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; AIDS; inflammatory disorder; developmental disorder; hypothyroidism;
                                                                                                                                                                                                                                                                                                                                                                                    New genomic sequence for cyanophage S-2L, useful for identifying genes for synthesis of 2,6-diaminopurine bases or polynucleotides containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; SECP; cytostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                Pochet S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                            Galisson F, Bouzon M, Robert C, Vico V;
(CNRS ) CNRS CENT NAT RECH SCI.
(GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55.5; DB Pred. No. 8; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein SECP-38 SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID NO 85; 423pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR56763 standard; protein; 136 AA.
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ACC79026 to ACC79105 encode the human secreted proteins (I) given in ABR56726 to ABR56805, designated SECP-1 to SECP-80. SECP sequences can have cytostatic, antiatreficestatic, anticonvulsant, antinflammatory, nootropic, neuroprotective, carebroprotective, anti-HIV, antiallargic and thyromimetic activities, and can be used in gene therapy. The SECP thyromimetic activities, and can be used in diagnosing, treating and proventing diseases or conditions associated with the decreased expression or overexpression of SECP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. ADIDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SECP. The SECP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polymcidetide, or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human secreted proteins (SECP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant SECP expression e.g. cancer, AIDS, atherosclerosis, Huntington's disease, stroke, infections.
                                                                                                                                                                                                                                                                                         Tang TY, Warren BA, Gietzen KJ, Lal PG, Yue H, Honchell CD, Lehr-Mason PM, Burford N, Xu Y, Baughn MR, Duggan BM, Tran UK, Lee EA, Forsythe IJ, Richardson TW, Lee S, Thangavelu K, Yue H, Emerling BM, Walia NK, Azimzai Y, Sanjanwala B, Hafalia AJA; Borowsky ML, Nguyen DB, Ison CH, Astromoff A, Ding L, Lee SY, Becha SD, Ramkumar J, Gandhi AR, Jin P, Fu GK, Swarnakar A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specifically bind to or modulate the activity of the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 217; 286pp; English.
                                                                               2001US-0324586P.
2001US-0343980P.
2001US-0334229P.
                   2001US-0317818P.
2001US-0317824P.
2001US-0324040P.
                                                                                                                                                                     06-MAR-2002; 2002US-0362439P.
2001US-0314752P
                                                                                                                                            2002US-0357002P
                                                                                                                                                                                      2002US-0366041P
                                                                                                                                                                                                            2002US-0376988P
                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-278569/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ACC79063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 136 AA;
                                                                                                   02-NOV-2001;
28-NOV-2001;
                                                                               24-SEP-2001;
                                       07-SEP-2001;
                                                             21-SEP-2001;
                                                                                                                                               13-FEB-2002;
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ABB92178;
 Query Match
            Best Loca
Matches
                                                                                                RESULT 15
                                                                                                          ABB92178
                                           ð
                                                               g
                      3
                     Gaps
                      3;
 DB 6; Length 136;
                      Indels
                    4;
Score 55.5; DB
Pred. No. 14;
1; Mismatches
                                                                                                                   AAY32836 standard; protein; 282 AA
                                        2 VWSSWAL--GWRWLRRYGWG 19
                                                             76 VW-WWPLNPGWRGLRRWOWG 94
43.0%;
                     Conservative
                                                                                                                                                              (revised)
Query Match
Best Local Similarity
                                                                                                                                                            17-0CT-2003
29-0CT-1999
                   12;
                                                                                                                                       AAY32836;
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Matches

RESULT 14 AAY32836

g

Arabidopsis thaliana

HBsAg; PreS2-S; recombinant antigen library; disease-related antigen; multivalent antigenic polypeptide production; infection; allergen;

Woodchuck hepatitis b virus HBsAg PreS2-S region protein sequence.

(first entry)

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This sequence is the woodchuck hepatitis virus surface antigen Pres2-S region. This sequence was used to create a recombinant antigen library comprises recombinant nucleic caids encoding antigenic polypeptides and is produced by recombination of at least two forms of nucleic acid, differing by at least two nucleotides, encoding a disease-recombinant multivalent polypeptides of the invention, that contains at least two antigenic polypeptides of the invention, that contains at least two antigenic polypeptides of the invention, that contains at least two antigenic polypeptides of the invention, that contains at least two antigenic polypeptides of the invention, that contains at least two antigenic polypeptides of the invention, that contains at least two antigenic polypeptides are used in vaccines to induce a protective or therapeutic response to a wide variety of infectious agents (bacteria, viruses, parasites, including plasmodium falciparum); allergens; asthma; autoimmune disease (e.g. rheumatoid arthritis, diabetes, multiple sclerosis); other inflammatory conditions and cancer, also, where directed against sperm antigens, they can be used for contraception. The multivalent peptides can be evolved to induce an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant multivalent antigenic polypeptide produced by recombining nucleic acid sequences and screening, used in vaccines against e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
asthma; autoimmune disease; rheumatoid arthritis; diabetes; therapy; multiple sclerosis; inflammatory condition; cancer; contraception; immune response; hepatitis b surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      optimised immune response against a wide variety of antigens, particularly a broad spectrum response to many different strains of pathogen, including strains that are likely to appear in the future.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 2; Length 282; Pred. No. 34; 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herbicidally active polypeptide SEQ ID NO 1389.
                                                                                                                                                                                                                                                                                                                                                                Howard R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 14; Fig 17; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                Whalen RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 SSWALGNYLWEWALARFSW 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SSWALG---WRW-LRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB92178 standard; protein; 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.6%;
                                                                                                                                                                                                       99WO-US002944.
                                                                                                                                                                                                                                            98US-00021769.
                                                                                                                                                                                                                                                             98US-0074294P.
                                                                                  Woodchuck hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infections and cancer
                                                                                                                                                                                                                                                                                                                                                                Bass SH,
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-518452/43.
N-PSDB; AAZ10971.
                                                                                                                                                                                                                                                                                                                         (MAXY-) MAXYGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 282 AA;
                                                                                                                                                                                                     10-FEB-1999;
                                                                                                                                                                                                                                            11-FEB-1998;
                                                                                                                        WO9941383-A1
                                                                                                                                                                                                                                                                                   23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                Punnonen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-2002
                                                                                                                                                                                                                                                                 11-FEB-1998
                                                                                                                                                               19-AUG-1999
        SXXXXXXXXXX
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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 1389; 261pp + Sequence Listing; English.
                                                                                     28-AUG-2001; 2001WO-EP009892.
                                                                                                                        28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                             Tietjen K, Weidler M;
                                                                                                                                                                                                                                 WPI; 2002-269010/31.
                                                                                                                                                          (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 452 AA;
                WO200210210-A2.
                                                  07-FEB-2002.
                                                                                                                                                                                                                                                                                                                        organisms.
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42.2%; Score 54.5; DB 5; Length 452; 56.2%; Pred. No. 64; cive 1; Mismatches 5; Indels 6 WALGWRWLRR-YGWGM 20 77 WTLGWSWAKREVIWGM 92 Query Match
Best Local Similarity 56.2
Matches 9; Conservative ò

1;

Gaps

1;

Search completed: October 26, 2004, 06:45:09 Job time : 86.5 secs

g

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Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 479, App
Sequence 479, App
Sequence 479, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 721, App
                                                                  ; Search time 64.25 Seconds (without alignments) 100.781 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 US-10-066-965A-2

4 US-10-066-965A-8

4 US-10-066-965A-1

4 US-10-066-965A-1

4 US-10-066-965A-1

5 US-10-424-59-149236

10S-09-1479

14 US-10-074-095-479

14 US-10-212-872-479

15 US-09-247-890-16

16 US-09-247-890-16

17 US-09-247-890-16

18 US-09-247-890-16

19 US-09-796-692-721

10 US-09-796-692-721
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                    1364641 segs, 323758627 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
                                                                   October 26, 2004, 06:45:25
                                                                                                                                        1 QVWSSWALGWRWLRRYGWGM 20
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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129
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Match Length DB
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1117
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56
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58
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                                                                                                                                                                                                                                                                                                                                 Database :
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Sequence 721, App	-	2808	ĭ	ĩ	4,	2	ĭ	equence 24	ਜ	H	m		15	7.5	609	199	Sequence 4332, Ap	70	1912	50652,	, Ap	۵				a)				84
US-10-	US-10-764-324-721	US-10-424-599-28	US-10-60	US-10-43	US-10-20	US-10-20	US-10-69	US-10-208-948-2	US-10-437-963-1804	US-10-437-963-13612	US-10-029-386-3227	US-10-425-114-5466	US-10-437-963-1	US-10-437-963-15654	-764-85	-764-B9	US-10-369-493-433	US-10-369-493	US-10-437-963-1912	US-10-282-122A-5065	US-09-812-86	US-10-437-9	US-10-437-9	US-10-437-5	09-864-76	US-10-437-963-2026	US-10-437-9	US-10-767-7	US-10-424-	US-10-437-963-18784
15	16	15	15	16	14	14	17	14	16	16	14	15	16	16	6	σ	14	14	16	15	σ	16	16	16	6	16	16	16	15	16
68	989	85	72	2094	11	15	15	15	123	65	105	152	191	537	242	242	410	410	239	261	346	513	539	104		118	Ŋ	П	251	9
	41.9																													
54	54	54	54	54	54	54	54	54	52.5	52	52	52	52	52	Н	m	51.5	П	51	51	51	51	51	50.5	20	20	20	20	20	20
14 7 1	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
                                                                                                   APPLICANT: COLAS, PIERRE
APPLICANT: COLAS, PIERRE
APPLICANT: COLAS, PIERRE
APPLICANT: COLBS, BAZAK A.
ITILE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: EGYP 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 129; DB 14; Length Best Local Similarity 100.0%; Pred. No. 8e-08; Matches 20; Conservative 0; Mismatches 0; Indels
                         Sequence 2, Application US/10066965A Publication No. US20030143626A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVWSSWALGWRWLRRYGWGM 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                               GENERAL INFORMATION:
US-10-066-965A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-066-965A-2
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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RESULT 2 US-10-066-965A-8 Sequence 8, Application US/10066965A ; Publication No. US20030143626A1

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APPLICANT: CONTAINED THERE
APPLICANT: BRENT, ROGER
APPLICANT: COHEN, BARAK A.
APPLICANT: COHEN, BARAK A.
TITLE OF INVENTION: TRAGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: BGYP 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COLAS, PIERRE
APPLICANT: BRENT, ROGER
APPLICANT: COHEN, BARAK A.
TILLOANT: COHEN, BARAK A.
TILL CON INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: EGYP 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILLING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: patentin Ver. 2.1
SEQ ID NO 7
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7. OTHER INFORMATION: Description of Artificial Sequence: Synthetic
1. OTHER INFORMATION: peptide
US-10-066-965A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                      Score 117; DB 14; Length 20; Pred. No. 1.7e-06;
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                                                                  US20030113749A1 Relevant
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Pred. No. 1.7e-06;
0; Mismatches 2;
                                                                                                                                                                                                                                       0; Mismatches
                                         TYPE: amino acid
STRAMPEDIESS: No. US20030113749,
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10066965A Publication No. US20030143626A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/10066965A Publication No. US20030143626A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    1 QVWSSWALGWRWLRRYGWGM 20
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SEQUENCE CHARACTERISTICS:
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.09
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Matches 18; Conservative
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                                                                                                                                          US-10-162-538-12
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                 APPLICANT: COLAS, PIERRE
APPLICANT: BRENT, ROGER
APPLICANT: COHEN, BARAK A.
TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: EGYP 3.0-015
CURRENT APPLICATION WIMBER: US/10/066,965A
CURRENT PILING DATE: 2002-12-09
NUMBER OF SEQ 1D NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
SEQ 1D NO 8
                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-066-965A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brent, Roger
McCoy, John M.
McSesen, Timm H.
Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 129; DB 14; Length 20; I Similarity 100.0%; Pred. No. 8e-08; 20; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEACHER PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,538
FILING DATE: 04-Jun-2002
CLASSIFICATION CURREN: US/08/630,052
RILNG DATE: UNKNOWN>
PRIOR APPLICATION NUMBER: US/08/630,052
FILING DATE: UNKNOWN>
PRIUSH DATE: CURROWN>
PRIUSH DATE: CURROWN>
APPLICATION NUMBER: US/08/630,052
FILING DATE: UNKNOWN>
PRIUSH DATE: UNKNOWN>
APPLICATION NUMBER: US/08/630,052
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REFERENCE/DOCKET NUMBER: 00786/311001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/278,082
FILING DATE: July 20, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTIONS
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                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Karen F. Lech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
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US-10-162-538-12
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Best Local
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2000-01-31
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thoush K
APPLICANT: Show Yihua
APPLICANT: Zhow Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (30)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 479
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 135;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.4%; Score 56; DB 9; Length 73; 47.1%; Pred. No. 28; 7; Indels tive 2; Mismatches 7; Indels
                    Indels
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US-10-424-599-149236
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Pred. No. 4.6;
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                  0; Mismatches
                                                                                                                                                                       Sequence 149236, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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50.0%; Pred
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                                                    1 QVWSSWALGWRWLRRYGWGM 20
                                                                                  1 OVWSLWALGWRWLRRYGWNM 20
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90.08;
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 similarity 90.0
18; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
''Loca 8; Conservat
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ORGANISM: Glycine max
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Best Local Similarity
Matches 9; Conserva
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NAME/KEY: SITE
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 Best Local
Matches 1
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC008C1
CURRENT APPLICATION UNMBER: US/10/074,095
CURRENT FILING DATIN: 2002-02-14
PRIOR APPLICATION NUMBER: 09/764,860
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/140,628
PRIOR PILLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-02-04
PRIOR PILLING DATE: 2000-02-04
PRIOR PILLING DATE: 2000-02-18
PRIOR PILLING DATE: 2000-07-11
PRIOR PELLOATION NUMBER: 60/220,963
PRIOR PELLOATION NUMBER: 60/220,963
PRIOR PELLOATION NUMBER: 60/220,963
PRIOR PELLOATION NUMBER: 60/220,963
PRIOR PELLING DATE: 2000-07-16
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR PELLING DATE: 2000-07-14
PRIOR PELLING DATE: 2000-08-14
PRIOR PELLING DATE: 2000-08-17
PRIOR PELLING DATE: 2000-09-27
Sequence 479, Application US/10074095 Publication No. US20030077704Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-17
APPLICATION NUMBER: 60/179,065
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FILING DATE: 2000-09-29
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APPLICATION NUMBER: 60/225,268
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A APPLICATION
R FILING DATE: 2000-09-25
R APPLICATION NUMBER: 60/229,343
R FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/229,345
TIME DATE: 2000-09-01
                                          R FILING DATE: 2000-09-29
R APPLICATION NUMBER: 60/251,856
R FILING DATE: 2000-12-08
R FILING DATE: 2000-12-08
R FILING DATE: 2000-12-08
R APPLICATION NUMBER: 60/251,868
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R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/237,038
R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/236,370
R FILING DATE: 2000-09-29
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R APPLICATION NUMBER: 60/237,040
R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/240,960
R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/239,935
R FILING DATE: 2000-10-13
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RR APPLICATION NUMBER: 60/225,213
RR FILING DATE: 2000-08-14
RR APPLICATION NUMBER: 60/227,182
RR FILING DATE: 2000-08-22
RR APPLICATION NUMBER: 60/225,214
RR APPLICATION NUMBER: 60/225,214
RR FILING DATE: 2000-08-14
RR APPLICATION NUMBER: 60/235,836
RR FILING DATE: 2000-09-27
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FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,287
...TMG DATE: 2000-09-01
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FILING DATE: 2000-10-13
APPLICATION NUMBER: 60/241,787
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/246,474
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APPLICATION NUMBER: 60/246,532
FILING DATE: 2000-11-08
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APPLICATION WUMBER: 60/249,210
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/226,681
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APPLICATION NUMBER: 60/249,218
FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/231,413
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APPLICATION NUMBER: 60/229,509
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APPLICATION NUMBER: 60/237,037
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APPLICATION NUMBER: 60/249,216
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APPLICATION NUMBER: 60/215,135
                      APPLICATION NUMBER: 60/236,368
FILING DATE: 2000-09-29
                                                                                                                                                                                                          FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/234,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/236,367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-09-29
FILING DATE: 2000-08-14
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                      PRIOR
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Gaps 0; Query Match
43.4%; Score 56; DB 14; Length 73;
Best Local Similarity 47.1%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 7; Indels APPLICATION DATE: 2000-11-1,
APPLICATION NUMBER: 60/249,211 Sequence 479, Application US/10212872; Publication No. US20030215893A1; GENERAL INFORMATION: APPLICATION NUMBER: 60/249,215 FILING DATE: 2000-11-17 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/232,400 APPLICATION NUMBER: 60/231,242 FILING DATE: 2000-09-08 FILING DATE: 2000-09-08
APPLICATION WINBER: 60/231,414
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/231,244 APPLICATION NUMBER: 60/246,475 FILING DATE: 2000-11-08 PRIOR APPLICATION NUMBER: 60/231,243 PRIOR FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/249,212 FILING DATE: 2000-11-17 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,244 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,214 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,297 APPLICATION NUMBER: 60/232,081 FILING DATE: 2000-09-08 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/232,080 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/233,064 APPLICATION NUMBER: 60/232,397 FILING DATE: 2000-09-14 APPLICATION NUMBER: 60/241,808 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/241,826 APPLICATION NUMBER: 60/241,786 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/241,221 APPLICATION NUMBER: 60/249,245 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,217 60/233,063 APPLICATION NUMBER: 60/232,399 60/232,401 APPLICATION NUMBER: 60/249,207 APPLICATION NUMBER: 60/249,264 2 VWSSWALGWRWLRRYGW 18 2000-09-14 2000-09-14 2000-09-14 2000-10-20 2000-10-20 2000-09-14 2000-09-14 16 IWSMWLPGEQWLRPXSW 2000-11-1 FILING DATE: 2000-09 APPLICATION NUMBER: FILING DATE: 2000-09 APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: US-10-212-872-479 PRIOR
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210 SSWALGNYLWEWALARFSW 228
            Bass, Steven H.
Whalen, Robert Gerald
Howard, Russell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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NAME/KEY: misc_feature
LOCATION: (30)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-212-872-479
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43.4%; Score 56; DB 14; Length 73;
Best Local Similarity 47.1%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 7; Indels
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC008C2
CURENT APPLICATION NUMBER: US/10/212,872
CURRENT FILING DATE: 2002-08-07
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 479
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 282;
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57.9%; Pred. No. 1.1e+02;
tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09247890
Publication No. US20020198162A1
GENERAL INFORMATION:
APPLICANT: Bunnonen, Juha
APPLICANT: Bass, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Arburion: Antigen Library Immunization
ITITLE OF INVENTION: Antigen Library Immunization
FILE REPRENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/247,890
CURRENT FILING DATE: 1999-02-10
EARLIER FILING DATE: 1999-02-11
EARLIER FILING DATE: 1998-02-11
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SECOTTANE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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Sequence 16, Application US/10383317
Publication No. US20040001849A1
GENERAL INFORMATION:
APPLICANT: Punnonen, Juha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 SSWALGNYLWEWALARFSW 228
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NAME/KEY: misc_feature
LOCATION: (70)
                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserval
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LENGTH: 282
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APPLICANT: Gagge, Alexander
APPLICANT: Gagger, Alexander
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITION OF STATES AND THERAPY
CURRENT APPLICATION NUMBER: 08/09/796,692
PRIOR PILING DATE: 2000-03-17
PRIOR PELING DATE: 2000-03-17
PRIOR PELING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR PELING DATE: 2000-05-04
PRIOR PELING DATE: 2000-06-04
APPLICANT: Howard, Russell APPLICANT: Howard, Russell APPLICANT: Stemmer, Willem P.C.
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Stemmer, Willem P.C.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US/09/247,890
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/074,294
PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-10
PRIOR PILING DATE: EARLIER FILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.6%; Score 55; DB 15; Length 282; 57.9%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Woodchuck hepatitis B virus
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Publication No. US20020198362A1
GENERAL INFORMATION:
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: Carter, Lauren
APPLICANT: Carter, Darricia Dianne
APPLICANT: Carter, Darricia Dianne
APPLICANT: Carter, Darricia Dianne
APPLICANT: Hematological Malignancies
TITLE OF INVENTION: Lematological Malignancies
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PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR PALICATION NUMBER: US 60/190,479

PRIOR PILLING DATE: 2000-03-01

PRIOR PLILING DATE: 2000-03-17

PRIOR PLILING DATE: 2000-04-27

PRIOR FILLING DATE: 2000-04-28

PRIOR FILLING DATE: 2000-04-28

PRIOR PLILING DATE: 2000-04-28

PRIOR PLILING DATE: 2000-05-07

PRIOR PLI
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CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
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; OTHER INFORMATION: Xaa = Any amino acid
US-10-057-4758-721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 721, Application US/10154884B; Publication No. US20040005561A1; Publication No. US20040005561A1
; APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                         Sequence 721, Application US/10057475B Publication No. US20040002068A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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3 WSSWA
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US-10-154-884B-721
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US-10-057-475B-721
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APPLICANT: Retter, Marc
CURRENT FILIAGO : Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014.058-0115.0016
FILE REFERENCE: 014.058-0115.0016
FILE REPERENCE: 014.058-0115.0016
FILE RETTER APPLICATION NUMBER: US 60/200, 745
FRIOR FILING DATE: 2000-04-08
FRIOR FILING DATE: 2000-04-08
FRIOR APPLICATION NUMBER: US 60/200, 999
FRIOR FILING DATE: 2000-05-01
FRIOR APPLICATION NUMBER: US 60/202, 084
FRIOR FILING DATE: 2000-05-01
FRIOR APPLICATION NUMBER: US 60/202, 903
FRIOR PELING DATE: 2000-05-04
FRIOR APPLICATION NUMBER: US 60/202, 416
FRIOR APPLICATION NUMBER: US 60/202, 416
FRIOR FILING DATE: 2000-08-03
FRIOR APPLICATION NUMBER: US 60/202, 378
FRIOR FILING DATE: 2000-08-04
FRIOR FILING DATE: 2000-08-04
FRIOR FILING DATE: 2000-08-04
FRIOR FILING DATE: 2000-08-04
FRIOR FILING DATE: 2000-08-03
FRIOR FILING DATE: 2000-08-04
FRIOR 
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                                                                                                                                                                                                                                                             Score 54; DB 9; Length 68; Pred. No. 43; 3; Indels 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        ---- LGWRWLRRYGWG 19
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CTHER INFORMATION: Xaa = Any amino acid
US-10-040-862-721
                                                           ; NAME/KEY: variant;
; LOCATION: (1)...(68)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-10-040-862-721
Sequence 721, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 41.9%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                     Best Local Similarity 27.0
Matches 10; Conservative
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                     Query Match
                                       FEATURE:
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us-10-066-965a-2.rapb

Algate, Paul A.

APPLICANT:

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APPLICANT: Adjace, Faul A, APPLICANT: Adjace, Faul A, APPLICANT: Adjace, Faul A, APPLICANT: Mannion, Jane APPLICANT: Marnion, Jane APPLICANT: Reter. Marc Mannion, Jane APPLICANT: Reter. Marc Mannion, Jane APPLICANT: Reter. Marc Compositions and Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy FILE OF INVENTION: Hemetological Malignancies
FILE REPERENCE: 014058-01322108
FILE REPERENCE: 014058-01322108
FRIOR APPLICATION NUMBER: US 60/186,126
FRIOR APPLICATION NUMBER: US 60/100,479
FRIOR APPLICATION NUMBER: US 60/200,303
FRIOR PELING DATE: 2000-04-28
FRIOR PELING DATE: 2000-04-28
FRIOR PELING DATE: 2000-04-28
FRIOR FILING DATE: 2000-05-01
FRIOR PELING DATE: 2000-05-01
FRIOR APPLICATION NUMBER: US 60/200,999
FRIOR FILING DATE: 2000-05-01
FRIOR APPLICATION NUMBER: US 60/200,999
FRIOR FILING DATE: 2000-05-01
FRIOR APPLICATION NUMBER: US 60/202,004
FRIOR APPLICATION NUMBER: US 60/202,004
FRIOR FILING DATE: 2000-05-01
FRIOR APPLICATION NUMBER: US 60/202,003
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-08-03
FRIOR 
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GRGANISM: Homo sapiens
FRATURE:

NAME/KEY: variant

JOCATION: (1)...(68)

GOTHER INFORMATION: Xaa = Any amino acid
US-10-154-884B-721
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Gaps

20;

|: || 8 WAPWAWGRCVTRFGLCREKIGSYGDLGWRWMRQHPAG 44

Search completed: October 26, 2004, 07:10:18 Job time : 64.25 secs

----LGWRWLRRYGWG 19

3 WSSWA---

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Query Match
Best Local Similarity
Matches 18; Conserv
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STATE: Massach
COUNTRY: USA
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32165, A
32165, A
16, Appl
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16, Appl
16, Appl
10, Appl
32359, A
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                                                                                                           2004, 06:20:00; Search time 22 Seconds (without alignments) 60.289 Million cell updates/sec
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2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-25051
US-09-247-890-16
US-09-724-969-16
US-09-724-969-16
US-09-724-95-16
US-09-95-91A-32359
US-09-560-385A-10
US-09-252-991A-32359
US-09-252-991A-32359
US-09-252-991A-32359
US-09-252-991A-31359
US-09-252-991A-31470
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US-09-193-104-26
US-09-489-039A-12110
US-09-252-991A-31085
US-09-2770-767-31648
US-09-270-767-86865
US-09-252-991A-32834
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US-09-252-991A-18571
US-09-252-991A-27351
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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129
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Match Length DB
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Perfect score:
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17, Appl
17, Appl
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17896, 1
20977, 1
18732, 1
25838, 1
22986, 1
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APPLICANT: Brent, John M.
APPLICANT: McCoy, John M.
APPLICANT: Jessen, Timm H.
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.7%; Score 117; DB 3; Length 20; 90.0%; Pred. No. Se-08; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/504,538A

FILING DATE: 07/20/95

CLASSIFICATION:
US-09-082-279B-1199
US-09-315-304B-1199
US-09-334-74-1199
US-09-515-966A-1199
US-09-350-641C-1199
US-09-252-991A-2199
US-09-252-991A-21965
US-09-252-991A-21965
US-09-252-991A-21965
US-09-252-991A-21996
US-09-252-991A-21896
US-09-252-991A-21896
US-09-252-991A-22996
US-09-252-991A-22996
US-09-252-991A-22996
US-09-252-991A-22996
US-09-252-991A-25938
US-09-252-991A-25938
                                                                                                                                                                                 US-08-655-704B-17
US-09-107-755-17
                                                                                                                                                                        US-09-291-922-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30,162
ER: 00786/259001
                                                                                                                                                                                                                                                                          US-08-504-538A-12; Sequence 12, Application US/08504538A; Sequence 12, Application US/08504538A; Patent No. 604746; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/278,082
                                                                                                                                                                                                                                                                                                                                                                                                E: Clark & Elbing LLP
176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
61LING DATE: 07/20/94
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
REFERENCE/DOCKET NUMBER: 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
   CORRESPONDENCE ADDRESS: ADDRESSE: Clark & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear US-08-504-538A-12
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2 VWSSWALG ----WRWLRRYGW 18
    NUMBER OF SEQUENCES: 20
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PCT-US95-09307-12
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APPLICANT: McCoy, John M.
APPLICANT: Lessen, Timm H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jessen, Timm H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR
TITLE OF INVENTION: DETECTING PROFILIN INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 00786/311001
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                    STALL
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WOTTER: IBM PC COMPALIble
"""TER: PC COMPALIBLE
""""TEM: PC COMPALIBLE
""""TEM: PC COMPALIBLE
""""TEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/278,082
FILING DATE: July 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application PC/TUS9509307
GENERAL INFORMATION:
                                                                                                                                   Sequence 12, Application US/08630052
Patent No. 6399296
                         1 QVWSSWALGWRWLRRYGWGM 20
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Boston
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-630-052-12
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GENERAL INCORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.2%; Score 57; DB 4; Length 382;
42.9%; Pred. No. 13;
tive 2; Mismatches 6; Indels
                                                                                                    COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version
SOFTWARE: #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00786/288001
                  ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32165, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00T
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OVWSSWALGWRWLRRYGWGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 542-5070
TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                             CITY: Boston
STATE: Massachusetts
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conserv
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Best Local Similarity
Matches 9; Conserv
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GENERAL INFORMATION:
APPLICANT: Bass, Steven H.
APPLICANT: Bass, Steven H.
APPLICANT: Bass, Steven H.
APPLICANT: Bass, Steven H.
APPLICANT: Wallen, Robert Gerald
APPLICANT: Wallen, Robert Gerald
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Asygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT PELING DATE: 2000-11-28
PRIOR PILING DATE: 1990-02-10
PRIOR PLING DATE: 1990-02-10
PRIOR PLING DATE: EARLIER FILING DATE: 1998-02-11
PRIOR PLING DATE: EARLIER FILING DATE: 1998-02-11
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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42.6%; Score 55; DB 4; Length 282;
Best Local Similarity 57.9%; Pred. No. 16;
Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 282;
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                                                          APPLICANT: Punnonen, Juha
APPLICANT: Punnonen, Juha
APPLICANT: Bass, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REPREMENCE: 018097-0289710US
CURRENT APPLICATION NUMBER: US/09/724,969
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/247,890
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: US 60/105,509
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Woodchuck hepatitis B virus
US-09-724-969-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Woodchuck hepatitis B virus
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US-09-724-852-16
; Sequence 16, Application US/09724852
...tont No. 6576757
Application US/09724969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 SSWALGNYLWEWALARFSW 228
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Best Local Similarity 57.9
Matches 11; Conservative
                     Patent No. 6569435
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 16
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44.2%; Score 57; DB 4; Length 1086;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
42.6%; Score 55; DB 4; Length 282;
1 Similarity 57.9%; Pred. No. 16;
11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bass, Steven H.
APPLICANT: Malen, Robert Gerald
APPLICANT: Howard, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Feemmer, Willem P.C.
APPLICANT: Stemmer, Marylem, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/247,890
CURRENT APPLICATION NUMBER: US/09/247,890
CURRENT APPLICATION NUMBER: US/09/247,890
CURRENT PILING DATE: 1998-02-10
EARLIER FILING DATE: 1998-02-11
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SEQTUARE: Patentin Ver. 2.0
SEQTUARE: 282
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CRGANISM: Woodchuck hepatitis B virus
US-09-247-890-16
                  106 VWSGWILAHETRWDWVGQLGW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09247890 Patent No. 6541011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 WSSWALGWRWLRRYGW 18
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APPLICANT: Punnonen, Juha

GENERAL INFORMATION:

US-09-247-890-16

RESULT 9

Query Match Best Local Similarity Matches 11; Conserva

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RESULT 7 US-09~724-969-16

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Mismatches
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TITLE OF INVENTION: Recombinant Laminin 5
FILE REPERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-WAR-1997
NAME: KOWALDER, THOMAS J. 147
REFERENCE/DOCKET NUMBER: 454310-299(
TELEPHONE: 212-588-0800
TELEPAX: 212-588-0800
TELEFAX: 212-588-0800
TELEFAX: 212-588-0800
TELEFAX: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454310-2990
      ZIP: 10151
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-560-385A-10; Sequence 10, Application US/09560385A; Patent No. 6703363
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Best Local Similarity 53.8%;
Matches 7; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           550 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: amino acid US-09-079-587-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 TGWRWGWRWLHQY 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 SSWALGWRWLRRY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 550 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-32359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Pate
SEQ ID NO 10
LENGTH: 1725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·,
                                                                                                                         APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: PARTINEZ, HECTOR
APPLICANT: PROUS, STEVEN B.
TITLE OF INVENTION: WECTORS HAVING ENHANCED EXPRESSION, AND
TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETII, ENZO
APPLICANT: PINCUS, STEVEN B.
APPLICANT: APPLICANT STEVEN B.
AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 2; Length 550;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elam PC compatible
COMPUTER: Elam PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,155B
FILING DATE: L2-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGBNT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REGISTRATION NUMBER: 32,147
REGISTRATION NUMBER: 32,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: PROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
Sequence 44, Application US/08816155B Patent No. 5990091
GENERAL INFORMATION:
APPLICANT: TARTAGLIA, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/09079587
Patent No. 6130066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEPAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 550 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | ||||| :|
524 TGWRWGWRWLHQY 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.0%
To Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                ADDA...
STREET: 745 CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: NE.
STATE: NEW YOUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-816-155B-44
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US-09-079-587-44
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    Sequence 32359, Application US/09252991A
    Patent No. 6551795
    GENERAL INFORMATION:
        APPLICANT: Marc J. Rubenfield et al.
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 4; Ler
Pred. No. 1.2e+02;
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILICATION NUMBER: US/09/079,587
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 3;
Pred. No. 41;
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GENERAL INCOMPANTION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.5%; Score 51; DB 5; 57.9%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.5%; Score 51; DB 4;
100.0%; Pred. No. 82;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                 00786/282001
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         APPLICATION NUMBER: PCT/US96/10602 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-31470
; Sequence 31470, Application US/09252991A
; Patent No. 6551795
                                                  CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017,814
FILING DATE: 20-JUN-1995
CLASSIFICATION:
ATTORNEY/ABROTI INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/2:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANS: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 SSWALGNYLWEWALARLSW 292
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                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           : 346 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.5
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein PCT-US96-10602-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 LGWRWLRR 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1099-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9146
LENGTH: 115
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR PLIING DATE: 1998-02-18
PRIOR PLIING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32359
LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                    Ouery Match 40.7%; Score 52.5; DB 4; Length 173; Best Local Similarity 58.8%; Pred. No. 21; Matches 10; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 115;
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GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Pred. No. 18;
                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 WSSWALGWRWLRRYGWG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 WSSRGSDWRWRRRC-WG 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 WALG-QWLRRKGFG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.9
Best Local Similarity 71.4
Matches 10; Conservative
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PCT-US96-10602-2
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CITY: BO
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Gaps

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Gaps ; 0 This Page Blank (uspto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 26, 2004, 06:19:49; Search time 17 Seconds (without alignments) 113.196 Million cell updates/sec

US-10-066-965A-3 Title: Perfect score:

118 1 PRGAPMWMRWVCQMLETMFL 20 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length	BB	QI	Description
п	49		429	7	G84176	ate dehydr
7	49		545	7	S23582	
£	48		359	Ŋ	AH3465	oxidoreductase (EC
4	48	40.7	435	H	S18609	glutamate dehydrog
S	47	39.8	382	7	C83337	- C
9		39.0	476	7	E72079	Ψ
7	46	σ	476	~	A86545	phospholipase D ty
8	46	ď.	777	7	865543	3',5'-cyclic-nucle
6	45	œ	099	7	H70798	probable cation-tr
10	45	œ	1123		S20497	phytochrome A - po
11	45	ω.	1191		AF2501	
12	44	37.3	194		AE3633	
13	44	7	264		AE2100	ത
14	44	7	350		T12260	caffeoyl-CoA O-met
15	44	7.	366		S40146	
16	44	7	370		B95420	probable sideropho
17	44	37.3	400	7	T25605	
18	44	7	463		T02481	probable protein k
19	44	37.3	499	ď	E86206	
20	44	7	200	~	T16630	hypothetical prote
21	44	7	Ŋ	N	T40518	major facilitator
22	44	7		7	S04401	spheroidene monoox
23	4	37.3	972	~	S77454	cation-transportin
24	43.5	9	277	7	T46209	hypothetical prote
25	43.5	36.9	570	N	T38489	~~1
26	ω.	36.9	614	N	D72373	hypothetical prote
27	43	36.4	106	(1	T44499	_
28	43	36.4	172	N	00	
29	43	36.4	368	(3	G86412	H

probable enzymes [probable enzymes y	probable membrane	related to cyclohe	hypothetical prote	probable enzyme yh	probable enzyme [i	hypothetical prote	RNA-directed DNA p	conserved hypothet	hypothetical prote	hypothetical prote	fructose-bisphosph	fructose-bisphosph	probable membrane	probable membrane
E90880	D85738	F64892	T49739	F70751	E86014	E91168	S47687	\$65818	B90266	T16479	T48538	139525	I39556	A70839	T36532
7	7	7	7	7	7	7	~	7	~	7	7	7	7	7	7
430	430	430	439	661	208	208	208	184	203	230	361	364	364	412	420
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36.4	36.4	36.4	36.4	36.4	36.(36.0	36.	35.	35.6	35.6	35.6	35.6	35.6	35.6	35.6
43 36.4	43 36.4	43 36.4	43 36.4			42.5 36.0		42 35.0	42 35.6	42 35.6	42 35.6	42 35.6	42 35.	42 35.	42 35.1

ALIGNMENTS

RESULT 1 G041717 G14172mate dehydrogenase [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004	R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liz A; Litle: Genome sequence of Halobacterium species NRC-1.	A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: G84176 A;Accession: 19429 estroy A;Betus: preliminary A;Alcecule type: DNA A;Residues: 1-429 estroy A;Alcecule type: DNA A;Residues: 1-429 estroy A;Alcecule type: DNA A;Residues: IA429 estroy A;Alcecule type: DNA A;Residues: IA429 estroy A;Alcecule type: DNA A;Residues: IA429 estroy A;Alcecule type: DNA A;Alcecule type: Alcecule type: Alce	A).Lettertences: Unitrol:QJDSM4; OB:ABOU443; NID:GLOS/9809; FIDN:AAG18/79.1; GSFDB:GFGCGS: C:Genetics: A,Gene: gdhB C;Superfamily: glutamate dehydrogenase (NAD(P)+) Query Match 429;	al Similarity 41.2%; pred. No. 37; Conservative 3; Mismatci 3 GAPMWRWVCQMLETMF 19 1
RESULT 1 G84176 glutamat C;Specie C;Date: C:Access	R;Ng, W.; Leitha, Jung, K Proc. Na A;Author A;Title:	A; Refere A; Access A; Status A; Molecu A; Residu	A; Closs Tele C; Genetics: A; Gene: gdhB C; Superfamil.	Best Loc Matches Oy Db

alpha-galactosidase (EC 3.2.1.22) precursor - Aspergillus niger

Apparations and the control of the c

A;Gene: aglA C;Superfamily: alpha-galactosidase

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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Jaccession: C8333
R;Stover, CK.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, I., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-382 <STO>
A;Cross_references: UNIPROT:Q91117; GB:AE004674; GB:AE004091; NID:g9948512; PIDN:AAG0585:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-476 <ARN>
A;Residues: 1-476 <ARN>
A;Cross-references: UNIPROT:Q9Z8A8; GB:AE001626; GB:AE001363; NID:g4376708; PIDN:AAD1857
A;Expeniental source: strain CWL029
C;Genetics:
A;Gene: CPn0435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: A86545
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Isl
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Isl
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Isl
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.; Fan, J.; Olinger, L.; Grimwood, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Chlamydophila pneumoniae (strain J138)
                                                        C83337
hypothetical protein PA2465 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pnospholipase D homolog - Chlamydophila pneumoniae (strain CWL029).
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, Nature Genet. 21, 388-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
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Pred. No. 16;
1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.8%;
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364 PLWKKWFCEKLK 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 PRGRPFWSKW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 5; Conserv
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-476 <STO>
                                                                                                                                                                                                                                                                                                                                                                     A,Accession: C83337
A,Status: preliminary
A,Molecule type: DNA
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A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: PA2465
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S18609
S18609
S18609
Glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Halobacterium salinarum
NiAlternene names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C;Species: Halobacterium salinarum
C;Date: 13-Jan-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: 186609
R;Benachenhou, N.; Baldacci, G.
Mol. Gen. Genet. 230, 345-352, 1991
A;Title: The gene for a halophilic glutamate dehydrogenase: sequence, transcription anal
A;Reference number: 518609; MUID:92114863; PMID:1766432
A;Accession: S18609
A;Molecule type: DNA
A;Residues: 1435 <-BEN>
A;Accession: Glate as Halobacterium salinarium
C;Superfamily: glutamate dehydrogenase (NAD(P) +)
C;Keywords: NADP; Oxidoreductase
F;126/Binding site: substrate (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                        AH3465

AH3465

Oxidoreductase (BC 1.1.1.-) [imported] - Brucella melitensis (strain 16M)

CiSpecies Brucella melitensis

CiDate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

CiAccession: AH3465

E; DelVecchio, V. G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Parvur, M.; Goltsman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

A; Reference number: AD3252; PMID:11756688

A; Status: preliminary

A; Status: preliminary
C;Keywords: glycoprotein; glycosidase; hydrolase
F1-31/Donalin: (or 9-11) signal sequence #status predicted <SIG>
F;32-545/Product: alpha-galactosidase #status experimental <MAT>
F;57,95,101,131,211,363,444/Binding site: carbohydrate (Asn) (covalent) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:Q8YP17, UNIPROT:Q8G2S3; GB:AE008917; PIDN:AAL52891.1; PID:gd
A,Experimental source: strain 16M
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                                                                                                                                           Length 545;
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                                                                                                                                                                                                    7; Indels
                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 2
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                       4; Mismatches
                                                                                                                                           Score 49;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PRGAP--MWMR-----WVCQMLE 16
                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                          1 PRGAPMWMRWVCQMLETMF 19
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                                                                                                                                                                                                                                                                                                               43 PMGFNNWARFMCDLNETLF
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Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                           41.5%;
                                                                                                                                         Query Match
Best Local Similarity 42.1
Matches 8; Conservative
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C, Keywords: oxidoreductase
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Best Local Similarity
Matches 11; Conserv
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A; Residues: 1-359 < KUR>
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Gaps

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4; Mismatches
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
'hea B; Conserve
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A;Residues: 1-1123 <HEY>
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A;Cross-references: FlyBase:FBgn0000479
A;Cross-references: FlyBase:FBgn0000479
A;Introns: 93/2; 125/3; 152/2; 165/2; 200/2; 262/3; 294/1; 407/3; 496/2; 534/2; 588/3; 7
A;Introns: 93/2; 2.5-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiester hydrolase
B;137-777/Product: cAMP-dependent 3',5'-cyclic-nucleotide phosphodiesterase, splice form
F;439-667/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
A;Cross-references: UNIPROT:Q928A8; GB:BA000008; NID:g8978807; PIDN:BAA98643.1; GSPDB:GN
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0435
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                                                                                                                                                                                                                                                                                                                                                                                                                            3,5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific, splice form II N;Contains: 3',5'-cyclic-nucleotide phosphodiesterase, cAMP-specific, splice form III S;Sepecies: Drosophila melanogaster (S;Species: Drosophila melanogaster (S;Date: 28-Oct-1995 #sequence revision 19-Jul-1996 #text_change 09-Jul-2004 (S;Accession: S65543; S19662; S65542; S65544; A26651 (S;Accession: S65543; S19662; S65542; S65544; A26651 (S;K.; Davis, R.L. J. Mol. Biol. 222, 553-565, 1991 (Mulp:) Biol. 222, 553-565, 1991 (Mulp:) Proposed Consophila melanogaster. A;Reference number: S19662; MUID:92085274; PMID:1660926
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70798
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A;Residues: 416-777 <CHE>
A;Cross-references: GB:M14982; NID:g157278; PIDN:AAC34201.1; PID:g157280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 'MQAEQ', 86-87,'IG',90-91,'QKYHSRYLKNRRHTLANVR',94-777 <Q13>
A;Cross-references: BMBL:X55174
A;Accession: S65544
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                                                                                                                                          Length 476;
                                                                                                                                                                                            Indels
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A,CCDen, C.N.; Denome, S.; Davis, R.L.
R;Chen, C.N.; Denome, S.; Davis, R.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 9313-9317, 1986
A;Title: Wolecular analysis of cDNA clones and the corre
A,Reference number: A26651; MUID:87092243; PMID:3025834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 'MVCSFCCCCXNFRN',4,'P',6,'S',94-777 <QI4>
                                                                                                                                          2;
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                                                                                                                                                                                            4; Mismatches
                                                                                                                                          Score 46; DB
Pred. No. 28;
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A; Accession: S19662
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                                                                                                                                       39.0%;
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A;Residues: 137-777 <212>
A;Cross-references: EMBL:X55174
A;Accession: &65542
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                                                                                                                                                                                                                                                                                 |:| :| :| 364 PLWKKWFCEKLK 375
                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                5 PMWMRWVCOMLE 16
                                                                                                                                       Query Match
Best Local Similarity
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nes 7; Conserv
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A; Residues: 1-777 <QIU>
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C;Accession: S20497
R;Heyer, A.; Gatz., C.
Plant Mol. Biol. 18, 535-544, 1992
Plant Mol. Biol. 18, 535-544, 1992
A;Title: Isolation and characterization of a cDNA-clone coding for potato type A phytochn A;Reference number: S20497; MUID:92163018; PMID:1536928
A;Accession: S20497
A;Accession: S20497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding dc F;33-386/Domain: ATPase transduction domain homology <ATT>
F;466-610/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
        . S.
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-660 <COL>
A;Cross-references: UNIPROT:069710; GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA1806
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295997; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromopurotein; phytochroeptor; phytochromobilin; transcription regulation
C;Keywords: chromopurotein; phytochrome homology <PHYTD:
F;323/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phytochrome A - potato
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 30-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 53;
1; Mismatches
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- common ice plant (fragment)

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Rinchalowski, C.B.; Bohnert, H.J.
Submitted to the EMBL Data Library, March 1998
A;Description: Mesembryanthemum crystallinum caffeic acid 3-0-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-350 <MIC>
A;Cross-references: UNIPROT:065362; EMBL:AF067968; NID:g3176966; PID:g3176967
                                                                                                                                                      caffeoyl-CoA O-methyltransferase (EC 2.1.1.104) - common ice plant (fragment
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Eucalyptus gunnii (oider tree)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S40146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-366 <GRI>
A;Cross-references: UNIPROT:P46484; EMBL:X74814; NID:9437776; PID:9437777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catechol O-methyltransferase (BC 2.1.1.6) - cider tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RiGrima-Pettenati, J.; Poeydomenge, O.; Boudet, A.M. submitted to the EMBL Data Library, August 1993 A;Reference number: S40146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Pathway: lignin biosynthesis
C; Superfamily: O-methyltransferase
C; Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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C,Keywords: methyltransferase; S-adenosylmethionine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: October 26, 2004, 06:46:24
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102 APSWLQWLANLLQ 114
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242 PKGDAIFMKWIC 253
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PKGDAIFMKWIC 269
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Best Local Similarity
Thad 5; Conserve
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                          A;Cross-references: UNIPROT:Q8YKV1, GB:BA000020; PIDN:BAB78274.1; PID:g17135728; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetial Source: at A;
A;Gene: alr7190
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphonate ABC transport permease protein phnB [imported] - Nostoc sp. (strain PCC 7120 5.5pecies: Nostoc sp. Brzain PCC 7120 5.5pecies: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 5.7Accession: AE2100 7.7NARAmura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; WUID:21595285; PMID:11759840 A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribelvecchio, v.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, F.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q8YBBO; UNIPROT:Q8FX32; GB:AE008918; PIDN:AAL54232.1; PID:g1
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            farnesyl cysteine carboxyl-methyltransferase BMEI10990 [imported] - Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb_2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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Pred. No. 24;
4; Mismatches
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                                                                                                                                                                                   DB 2;
                                                                                                                                                                                 Score 45; DB 2
Pred. No. 91;
4; Mismatches
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40.0%;
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Best Local Similarity 42.2.
Best Local 6, Conservative
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Best Local Similarity
A;Residues: 1-1191 <KUR>
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
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A;Map position: II
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Gaps

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Indels

Length 350;

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Score 44; DB Pred. No. 42; 5; Mismatches ·.

Gaps

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Length 366; 2; Indels

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Q8ftc3 corynebacte
Q9xeq3 sorghum bic
Q91rr5 arabidopsis
Q60716 human immun
Q7uky1 rhodopirell
Q93hk1 streptomyce
Q82776 streptomyce
Q91117 pseudomonas
Q91011 pseudomonas
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Q8h727 phytophthor
Q9z8a8 chlamydia p
                                                                                                                                                                                                                                                                                                                                                              Q82q22 streptomyce
Q8idr5 plasmodium
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Q8mrn3 drosophila
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Q7w0a6 bordetella
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                                                October 26, 2004, 06:09:56; Search time 93 Seconds (without alignments) 123.736 Million cell updates/sec
                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q8ftc3
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5.1.6
Compugen Ltd.
                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                          1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                     Q7RP82
DHE4_HALN1
AGAL_ASPNG
Q8G2S3
Q8YF17
GenCore version Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9XEQ3
DR21 ARATH
Q6E716
                                                                                                                                                                                                                                                                                                                                                                                                                                              DHE4 HALSA
QBFTC3
                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                 using sw model
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Q7U9Z7
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                                                                                                  1 PRGAPMWMRWVCQMLETMFL 20
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091117
070IN1
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Q61699
Q82Q22
Q81DR5
Q73YY9
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Q7S1Z4
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Q93HK1
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                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                  US-10-066-965A-3
                                                                                                                                                                                                                                                                                                                      Query
Match Length DB
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1424
861
209
251
260
382
                                 - protein search,
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50.5
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50
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Perfect score:
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Maximum DB
                                  OM protein
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                                                 Run on:
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Q7wg61 bordetella	Q8iru6 drosophila	Q8iru4 drosophila	Q9w4s8 drosophila	Aaf45865 drosophil	P12252 drosophila	Q8iru5 drosophila	Aan09605 drosophil	Q8fpg2 corynebacte	Q9w4t0 drosophila	Aaf45862 drosophil	Q9w4s9 drosophila	Aaf45863 drosophil	Q9w4t1 drosophila
Q7WG61	QBIRUG	Q8IRU4	Q9W4S8	AAF45865	CNA1 DROME	QBIRŪS	AAN09605	Q8FPG2	Q9W4T0	AAF45862	Q9W4S9	AAF45863	Q9W4T1
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629	642	662	701	701	777	814	814	875	903	903	983	983	1057
39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0	39.0
		9	46	46	46	46	46	46	46	46	46	46	46
46	46	7											

ALIGNMENTS

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-!- MISCELLANDROUS: The sequence shown here is derived from an EMBL, Genbank/DDBJ third party annotation (TPA) entry.

EMBL, BK002744; DAA04249:1; A7401824148BA72D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                                ORFNames=HDC14914;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces griseus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                         44.9%; Score 53; DB 2; Length 185; 75.0%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Kato J., Chi W., Ohnishi Y., Hong S., Horinouchi S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB182575; BAD24658.1; -..
NON_TER
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27, Last annotation update)
                                                                     Last sequence update)
Last annotation update)
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NCBI_TaxID=1911;
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                          185 AA
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                                                        Created)
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                          PRT;
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                                                       27,
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Best Local Similarity 75...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 WMRWVCQMLETM 18
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                          PRELIMINARY;
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                                                       05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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                                                                                                                                                                                                                         SEQUENCE FROM N.A. PubMed=14709175;
                                            Q61JH2;
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                          Q61JH2
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Q61699
RESULT 1
              Q61JH2
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE FROM N.A.
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05-JUL-2004
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  Q8IDR5;
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Nat. Biotechnol. 21:526-531(2003).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                          Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.8%; Score 50.5; DB 2; Length 307; 56.2%; Pred. No. 19;
                                                                                 4; Indels
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SEQUENCE 307 AA; 32843 MW; 2AE470395BAD60C4 CRC64;
159 AA; 17359 MW; 2D006A96A1A2B860 CRC64;
                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SDR) family.

EMBL; AP005023; BAC68409.1; -
HSSP, 070351, 1E32,
GO, GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR002198; ADH short.
InterPro; IPR002347; Adh short. C2.
InterPro; IPR002453; Beta_tubulin.
PRINTS; PR00061; GDHRDH.
PRINTS; PR00061; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycineae; Streptomycetaceae; Streptomyces.
                                        DB 2;
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PROSITE; PS00228; TUBŪLIN_B_AUTOREG; UNKNOWN_1.
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                                      42.8%; Score 50.5; DE 56.2%; Pred. No. 9.8; tive 2; Mismatches
                                                                                                                                                                                                                                                                  307 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                            96 APPWLRW-COPLRPLF 110
                                                                                                                     4 APMWMRWVCQMLETMF 19
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                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 24, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=SAV699;
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces avermitilis.
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                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                  Putative oxidoreductase.
                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                   Q82Q22;
01-JUN-2003
01-JUN-2003
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SEQUENCE
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QRIDRS
ID QRIDRS
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Matches
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
Berriann M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AL844509; CAD52554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GO; GO:0005956; C:protein kinase CK2 complex; IEA.

GO; GO:0016301; P:kinase activity; IEA.

GO; GO:0016805; F:protein kinase CK2 regulator activity; IEA.

InterPro; IPR000704; CAS kinase_II.

Pfam; PF01214; CK_II_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AE017233, AAS04131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium avium complex (MAC).
                                                                                                          Name=PF13 0232;
Dlasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 AA; 45284 MW; 9972EB55BCB6EF87 CRC64;
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                              01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Casein kinase II regulatory subunit, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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ب
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42.9%; Pred. No. 28;
iive 4; Mismatches
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SEQUENCE 459 AA: 49141 MW: SE3BD1C2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009059; bi resp regitr C. InterPro; IPR009043; RNA pol_sigma. InterPro; IPR007627; sigma70_r2. InterPro; IPR007630; Sigma70_r4. Pfam; PF04542; Sigma70_r4; 1.
     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00472; CASNKINASEII
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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161 WIEWFCQLKQNLFL 174
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OrderedLocusNames=MAP1814;
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Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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RESULT 6 AAS04131

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MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797; MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797; MGDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797; Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Meir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz K., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., "Genome sequence of Halobacterium species NRC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                       Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Petterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergam L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 44, Last annotation update)
NADP-specific glutamate dehydrogenase B (BC 1.4.1.4) (NADP-GDH B).
Name-gdhB; OrderedLocusNames=VNG0161G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasite Plasmodium yoelii yoelii.";
Nature 411:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
-EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AABLO1000421; EAA20924.1; -.
GO; GO:0005956; C:protein kinase CK2 complex; IEA.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0006605; F:protein kinase CK2 regulator activity; IEA.
InterPro; IFR000704; CAS kinase_II.
Pffan; PF01214; CK1 Lbeta; 1.
PRINTS; PR00472; CASNKINASEII.
                                                                                                                                                                                     Eukaryota; Ālveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081)
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01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.5%; Score 49; DB 2;
Best Local Similarity 42.9%; Pred. No. 36;
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                                                                                         Casein kinase ii beta chain.
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126 WIEWFCQLKQNIFL 139
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                                                                                                                                                       Plasmodium yoelii yoelii
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=73239;
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                                                                                                                                                                                                                                                                                                                                                PubMed=12368865;
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                                                                                                                          Name=PY01577;
                                                                                                                                                                                                                                                                                                                  STRAIN=17XNL
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Chain P., Lamerdin J.E., Regala W., Allen B.E., McCarren J.,
Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).
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EMBL; AE017233; AAS04131.1; -.
                                                                                                                                                                                                                                                                                                               Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943; MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.4%; Score 50; DB 2; Length 459; 63.6%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 459 AA; 49141 MW; 5E3BD1C2DE326095 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E4D8440C13387E35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechococcus sp. (strain WHB102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=84588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                            Last sequence update)
Last annotation update)
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57.1%; Pred. No. 32;
live 2; Mismatches
                                                                                            459 AA.
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GO; GO:0003824; F: catalytic activity; IEA.
InterPro; IPR000073; A/b_hydrolase.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00561; Abhydrolase 1; 1.
Complete proteome; Hypothefical protein.
SEQUENCE 311 AA; 34579 MW; E4D8440C133
                                                                                                                                                           Created)
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                                                                                                                                                    02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, Hypothetical protein. MAP1814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=SYNW0105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 PAWMTWVRPLLKTM 169
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les 7, Conservative
                                                                                            PRELIMINARY;
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1770;
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AAS04131;
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RESULT 7

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Best Loc Matches

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c. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate
                                                          + NH(3) + NADPH.
SUBUNIT: Homohexamer (By similarity).
SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to family 27 of glycosyl hydrolases. SIMILARITY: Contains 1 ricin B-type lectin domain. CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
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STRAINS-ATCC 9089 / N402;
MEDLINE=92318893; PubMed=1320186;
MEDLINE=92318893; PubMed=1320186;
Men Herder I.F., Rosell A.M.M., van Zuilen C.M., Punt P.J.,
van den Hondel C.A.M.J.J.;
"Cloning and expression of a member of the Aspergillus niger gene
"Cloning and expression of a member of the Aspergillus niger gene
family encoding alpha-galactosidase.";
Mol. Gen. Genet. 233:404-410(1992).
-!- FUNCTION: Represents a minor extracellular alpha-galactosidase
activity in A.niger.
-!- CATALYTIC ACTIVITY: Melibiose + H(2)O = galactose + glucose.
-!- PTM: A C-terminal Ser/Thr-rich region may provide possible sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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01-DEC-1992 (Rel. 24, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Alpha-galactosidase A precursor (EC 3.2.1.22) (Melibiase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
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A344F09C60BE60A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.5%; Score 49; DB 1;
41.2%; Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; G84176; G84176.

PIRSPP, P96110; 1B3B.

InterPro; IPR006095; GLFV dehydrog.

InterPro; IPR006095; GLFV dehydrog_C.

InterPro; IPR006097; GLFV dehydrog_N.

InterPro; IPR006097; GLFV dehydrog_N.

InterPro; IPR00205; NAD BS.

Pfam; PF02812; GLFV_dehydrog; 1.

PRINTS; PR02812; GLFV_dehydrog N; 1.

PRINTS; PR00082; GLFDHPRGNASE;

PROSITE; PS00074; GLFV_DEHYDROGENASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; NAD\overline{\rm P}_i Oxidoreductase ACT_SITE 119 By similari
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GLSMWMTWKCAVMDLPF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004982; AAG18779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 AA; 45968 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAPMWMRWVCQMLETMF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 41.2.
7; Conservative
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P28351;
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  and for commercial
                    (See http://www.isb-sib.ch/announce/
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                                                                                                        PIR; $23582; $23582.

R GlycoSuiteDB; P28351; -
R InterPro; IPR00241; Glyco hydro_27.

R InterPro; IPR0011; Glyco hydro_GHD.

R InterPro; IPR0011; Glyco hydro_GHD.

R InterPro; IPR0011; RicinE_lectin.

P Fam; PF00652; Ricin B lectin; 3.

R PRINTS; PR00740; GLIYDRIASE27.

R PROSTIF; PS00512; ALPHA GALACTOSIDASE; 1.

R PROSTIF; PS00521; RICIN_ELECTIN; 1.

R PROSTIF; PS00521; ALPHA GALACTOSIDASE; 1.

R PROSTIF; PS00512; ALPHA GALACTOSIDASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proton donor (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
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Ricin B-type lectin.
Nucleophile (By similarity)
Usage by
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(GlcNAc. . .)
(GlcNAc. . .)
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
EMBL; AE014337; AAN29190.1; -.
PIR; AH3465; AH3465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
By similarity.
N-linked (GlonAc.)
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modified and this statement is not removed.
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                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.5%; Score 49;
                         entities requires a license agreement
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01-0707-2003 (TrEMBLrel. 24, Last ann
Oxidoreductase, Gfo/Idh/MocA family.
OrderedLocusNames=BR0241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                              EMBL; X63348; CAA44950.1; -.
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STRAIN=1330 / Biovar 1;
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545
162
220
220
220
164
101
131
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363
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tes 8; Conserv
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SO WE WE WAY

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MEDLINE=22723752; PubMed=12840036;
                                     MEDLINE=92114863; PubMed=1766432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 AA; 47458 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X63837; CAA45327.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S18609; S18609.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=152794;
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          SEQUENCE FROM N.A.
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                                                                                                                                                PubMed=12052548;
                            STRAIN=CCM 2090;
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Matches
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                                                                                                                                                Gaps
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01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
NAD-specific glutamate dehydrogenase (EC 1.4.1.2) (NAD-GDH).
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.7%; Score 48; DB 2; Length 359; 45.8%; Pred. No. 52;
                                                                                                                 40.7%; Score 48; DB 2; Length 359;
45.8%; Pred. No. 52;
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                                                                                                                                                3; Indels
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                                                                                    359 AA; 39386 MW; 21CA7CDB75AEB2E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 AA; 39386 MW; 21CA7CDB75AEB2E5 CRC64;
                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Orderedingnam...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)
EMBL; AE009605; AAL52891.1; -.
         GO; GO:0016491; F:oxidoreductase activity; IEA GO; GO:0006118; P:electron transport; IEA. InterPro; IPR000683; GFO/IDH/MocA.N. PF01408; GFO_IDH_MocA; 1.
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                                                                                                                                                  2; Mismatches
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                                                                                                                                                                                                          276 PRGEPDELWIRPKGGDDWVCVPLE 299
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                                                                                                                                                                              1 PRGAP--MWMR-----WVCQMLE 16
                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                               45.8%;
                                                                                                                                                  11; Conservative
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                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                             Brucella melitensis.
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                                                                                                                                  Best Local Similarity
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                                                                     Complete proteome
SEQUENCE 359 AA
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                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                      Hayden B.M., Bonete M.J., Brown P.E., Moir A.J., Engel P.C., "Glutamate dehydrogenase of Halobacterium salinarum: evidence that the
                                                                                                                                                                                                                                                                                                                                 gene sequence currently assigned to the NADP+-dependent enzyme is in fact that of the NAD+-dependent glutamate dehydrogenase."; FEMS Microbiol. Lett. 211:37-41(2002).
-!- CATALYTIC ATTULYTY: L-glutamate + H(2)0 + NAD(+) = 2-oxoglutarate + NH(3) + NADH.
-!- SUBUNIT: Homohexamer (By similarity).
-!- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                            SEQUENCE OF 119-128; 184-193 AND 268-276, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
Benachenhou N., Baldacci G.,
"The gene for a halophilic glutamate dehydrogenase: sequence, transcription analysis and phylogenetic implications.";
Mol. Gen. Genet. 230:345-352(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 435;
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0E4E940D2FF8B9D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter TetB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct protein sequencing, NAD, Oxidoreductase. ACT_SITE 126 126 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 40.7%; Score 48; DB ilarity 41.2%; Pred. No. 63; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF0212; GLFV_dehydrog N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P96110; 1B26.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV dehydrog_C.
InterPro; IPR006097; GLFV dehydrog_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=tetB; OrderedLocusNames=CE1646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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ALL GENOME RES. 13:1572-1579(2003).

C. I-SIMILARITY: Belongs to the ABC transporter family.

REMEL; AP005219; BAC18456.1; -.

REMEL; AP005219; BAC18456.1; -.

REMEL; AP005219; BAC18456.1; -.

REMEL; AP005219; BAC18456.1; -.

RO; GO:0004009; F:ATP binding; IEA.

GO; GO:0004009; F:ATP-binding; IEA.

GO; GO:0004009; F:ATP-binding; IEA.

GO; GO:0004009; F:ATP-binding; IEA.

RO; GO:0006166; F:ATP-binding; IEA.

RO; GO:0000166; F:ATP-binding; IEA.

RO; GO:0000166; F:ATP-binding; IEA.

RO; GO:0000166; F:ATP-binding; IEA.

RO; GO:0004309; AAA ATPRASE.

RITERPRO; IPR001187; ABC membrane 1.

RITERPRO; IPR001187; ABC membrane 1.

RITERPRO; IPR001499; ABC transporter.

REMEM; PR000064; ABC transporter; 1.

RODOM; PD0000066; ABC transporter; 1.

RODOM; PD0000066; ABC transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
"Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UON-2003 (TrEMBLrel. 24, Last annotation update)
01-UON-2003 (TrEMBLrel. 24, Last annotation update)
H beta 5B homolog (Sorghum) (Sorghum vulgare).
Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
NCBL TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Query Match

40.7%; Score 48; DB 2; Length 612;
Best Local Similarity 47.1%; Pred. No. 88;

Matches 8; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
40.7%; Score 48; DB 2; Length 616;
Best Local Similarity 43.8%; Pred. No. 89;
Matches 7; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Lidaca V., Lou A., Young S., Messing J.;
Lulaca V., Lou A., Young S., Messing J.;
Submitted (1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF114171, AAD27568.1;
EMBL, AF114171, AAD27568.1;
InterPro; IPRO05377; Vps26.
Pfam, PRO3643, Vps26, Vps26.
SEQUENCE 616 AA; 70275 MW; 6BC1F53E929A70A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50929; ABC_TM1F; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete proteome.
SEQUENCE 612 AA; 64841 MW; 4CB9EA0B23F78D51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 RGSPAYVRWFPEGLDTM 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                            efficiens.";
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RATURE COURT COURT
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Search completed: October 26, 2004, 06:39:23 Job time : 96 secs

|| :|:|| : |: | 89 GARLWLRWAMKPLQAM 104 3 GAPMWMRWVCQMLETM 18

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Gaps

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us-10-066-965a-3.rag

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Page

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

2004, 06:09:56 October 26, Run on:

; Search time 85.5 Seconds (without alignments) 83.913 Million cell updates/sec

US-10-066-965A-3 Title: Perfect score:

Sequence:

2002273 seqs, 358729299 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp2000s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2003s:*
geneseqp2003bs:*
geneseqp2003bs:* A_Geneseq_23Sep04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ok			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length	DB	ΠD	Description
	49	41.5	441	2	AAR70209	Aar70209 A. niger
7	48.5	41.1	47	4	ABB38152	Abb38152 Peptide #
m	48.5	41.1	47	4	AAM31580	Aam31580 Peptide #
4	48.5	41.1	47	4	ABB23358	Abb23358 Protein #
S	48.5	41.1	47	4	AAM71301	Aam71301 Human bon
9	48.5	41.1	47	4	AAM58788	Aam58788 Human bra
7	48.5	41.1	47	4	ABG53012	Abg53012 Human liv
8	48.5	41.1	47	ın	ABG41101	Abg41101 Human pep
σ	48	40.7	96	ო	AAY56647	
10	48	40.7	98	S	AA021796	Aao21796 Lung-spec
11	. 48	40.7	140	m	AAY56712	Amind
12	47	39.8	318	4	ABG15007	Abg15007 Novel hum
13	47	39.8	421	7	AB083694	Pseuc
14	46.5	39.4	336	4	ABG08345	Abg08345 Novel hum
15	46	6	102	7	ADE72560	
16	46	39.0	116	N	AAR66340	Aar66340 Human imm
17	46	39.0	196	6	AAY35036	Aay35036 Amino aci
18	46	39.0	476	Ŋ	ABB90563	Abb90563 Chlamydia
19	46	σ	624	4	ABB59475	Abb59475 Drosophil
20	46	39.0	629	9	ABU23308	Abu23308 Protein e
21	45.5	ъ.	718	ထ	ADM92105	Adm92105 S pneumon
22	45	8	129	S	ADK36943	Adk36943 Novel hum
23	45	38.1	m	4	AAU52383	Aau52383 Propionib
24	45	38.1	136	9	ABM48902	Abm48902 Propionib
25	45	38.1	1119	4	ABB63999	Abb63999 Drosophil

Aau55294 Propionib Abm51813 Propionib Adi21546 Novel hum	Abg27818 Novel hum Adi21055 Novel hum Adn47433 Thermococ	Adm04382 Human pro Aag25276 Arabidops		Aag47428 Arabidops Aag47427 Arabidops Aag25597 Arabidops		Aag25596 Arabidops Abb93811 Herbicida	Adn73605 Thale cre Aao30114 Strawberr
AAU55294 ABM51813 ADI21546	ABG27818 ADI21055 ADN47433	ADM04382 AAG25276 AAG25275	AAG25598 AAG25274	AAG47428 AAG47427 AAG25597	ADK39715 AAG47426	AAG25596 ABB93811	ADN73605 AAO30114
467	4 1 8	7 m m	1 M M	m m m	, co m		8 9
63 63 140	152 231 292	308	330	330 340 440	3.4.8	363 363	363 365
37.3 37.3 37.3	37.3 37.3 37.3	37.3	37.3	37.3	37.3		37.3
4 4 4 4 4 4	4 4 4 4 4 4	4 4 4	4 4 4 4 4	4 4 4	4 4	4 4	4 4 4 4
26 23 28		3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	# 55 99 90 P2 #	37 38 39	4 4 7 0 11	42 43	44 45

ALIGNMENTS

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DNA encoding coffee bean alpha-galactosidase (CBG) was obtained by isolating mRNA from coffee beans, prepg. cDNA and subjecting this to PCR amplification using primers based on the amino acid sequence of CBG. A full-length cDNA clone is given in AAQ83523, which encoded a 42 kDa protein (AAR70205). Recombinant CBG was produced in Sf9 cells. CBG showed homology to alpha-galactosidases from guar, human placenta, S. cerevisiae and A. niger (AAR70206-09). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant coffee bean alpha-galactosidase - used for cleaving alphal, 3-linked galactose residues on the surface of cells for prodn. blood prods.
                                                                                                                                                      Alpha-galactosidase; coffee bean; CBG; alpha-1,3-linked galactose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 49-50; 67pp; English.
                          AAR70209 standard; protein; 441 AA.
                                                                                                                                                                                                                                                                                                                                             (NYBL-) NEW YORK BLOOD CENT INC.
                                                                                                                                                                                                                                                                                                                93US-00118470.
                                                                                                                             A. niger alpha-galactosidase.
                                                                                                                                                                                                                                                                                    94WO-US009662.
                                                                                   (revised)
(first entry)
                                                                                                                                                                       antigen; blood group.
                                                                                                                                                                                                                                                                                                                                                                         Goldstein J;
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-123231/16.
                                                                                                                                                                                                  Aspergillus niger.
                                                                                                                                                                                                                                                                                    26-AUG-1994;
                                                                                                                                                                                                                                                                                                                08-SEP-1993;
                                                                                                                                                                                                                              WO9507088-A1
                                                                                                                                                                                                                                                         16-MAR-1995.
                                                                                   25-MAR-2003
21-SEP-1995
                                                       AAR70209;
                                                                                                                                                                                                                                                                                                                                                                         Zhu A,
RESULT 1
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5

Length 441;

Score 49; DB 2; Pred. No. 49;

41.5%;

Query Match Best Local Similarity

Sequence 441 AA;

ABB38152

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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein #5357 encoded by probe for measuring heart cell gene expression.
                 Peptide #5617 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.1%; Score 48.5; DB 4; Length 47; 60.0%; Pred. No. 6.6; ive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                   Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 31849; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB23358 standard; protein; 47
                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                    2000US-0180312P.
2000US-0207456P.
2000US-060840B.
2000US-00632366.
2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000666.
                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                        2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                    qenetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47 AA;
                                                                                                                                   WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157274-A2
                                                                                                                                                                                                                                                                                     03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                      26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing
 Gaps
                                                                                                                                                                                                                                                                                     expression; single exon nucleic acid probe.
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 ö
                                                                                                                                                                                                                                                    Peptide #5658 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 30787; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48.5; DB 4; Length 47; Pred. No. 6.6;
 Indels
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7;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank
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                                                                 61
                                 PRGAPMWMRWVCQMLETMF 19
 4;
                                                                                                                                                   ABB38152 standard; peptide; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                 PMGFNNWARFMCDLNETLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.18;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000GB-00024263
                                                                                                                                                                                                                                                                                  Human; foetal liver; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                   (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 60.0
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                       WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                   04-FEB-2002
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8;
                                 Н
                                                                 43
                                                                                                                                                                                     ABB38152;
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Matches
                                                                                                                  RESULT 2
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AAM31580

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Gaps

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain expressed single exon probe encoded protein SEQ ID NO: 30893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                          Example 4; SEQ ID NO 31607; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                        41.1%; Score 48.5; DB 4; Length 47; 60.0%; Pred. No. 6.6; tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR
            DR;
            Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM58788 standard; protein; 47 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PRGAPMWMRWVCQMLETMFL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||
|3 PRGAPNLGAWVLQCLE-IFL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MXY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
27-SEP-2000; 2000US-0234587P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483446/52
                Hanzel DK,
                                                  WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                             Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM58788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                           probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, the hyperension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535_ABA41305). The present sequence is a protein encoded by one such
                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bone marrow expressed probe encoded protein SEQ ID NO: 31607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.1%; Score 48.5; DB 4; Length 47; 60.0%; Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                   Claim 15; SEQ ID NO 25128; 530pp; English
                                                                                                                                                                                               Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM71301 standard; protein; 47 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRGAPMWMRWVCOMLETMFL 20
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|PRGAPNLGAWVLQCLE-IFL 31
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
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2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312P.
                                                                                                                                                                                                 Chen W,
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                    26-MAX-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060B408.
03-AUG-2000; 2000US-0363366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                             03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
24-SEP-2000; 2000US-0234558P.
04-OCT-2000; 2000GB-00024263P.
      2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 12; Conserv
                                                                                                                                                                                                                                        WPI; 2001-488899/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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        04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                     hearts.
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Matches
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Gaps

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Indels

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Mismatches

., H

Conservative

12;

Matches

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1 PRGAPMWMRWVCQMLETMFL 20

31

PRGAPNLGAWVLQCLE-IFL

13

RESULT 8 ABG41101 Human peptide encoded by genome-derived single exon probe SEQ ID 30766.

(first entry)

19-AUG-2002

ABG41101;

ABG41101 standard; peptide; 47 AA

chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyspiasia; primary ciliary dyskinesis; pulmonary hypertension;

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1;
  epilepsy and cancers. The present sequence is a protein encoded by one of
the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe (SENP) (I) for
                                                                       Gaps
                                                                                                                                                                                                                                 Human; liver; cirthosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                      1;
                                                                     Indels
                                                   4; Length
                                                                    ; 9
                                                41.1%; Score 48.5; DB
60.0%; Pred. No. 6.6;
ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 31660; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                              Human liver peptide, SEQ ID No 31660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression in human adult liver
                                                                                                                                                      ABG53012 standard; peptide; 47 AA
                                                                                    1 PRGAPMWMRWVCOMLETMFL 20
                                                                                                         31
                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                   13 PRGAPNLGAWVLOCLE-IFL
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                             2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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2000US-00632366.
                                                                                                                                                                                                                                                                                                                                         2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                   2000US-0207456P
                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                               entry)
                                                                    Conservative
                                                                                                                                                                                                                                Human; liver; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG, Hanzel DK,
                                                                                                                                                                                             (first
                                                        Local Similarity
Les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488898/53
                            Sequence 47 AA;
                                                                                                                                                                                                                                                                                WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
 epilepsy and
                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
                                                                                                                                                                                             25-FEB-2003
                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                               Query Match
                                                                                                                                                                         ABG53012;
                                                                Matches
                                                                                                                                    RESULT 7
                                                                                                                                              ABG53012
8 X 8 8
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mucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12887 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes with the human lung, comprising the novel set of probes with the human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array, identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (a) a glgorithmically predicting at least one exon from general exon probe, contacting a fragment identical to the predicted exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) measuring the expression of each of the exons in several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a spatially-addressable set of single exon
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measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification for complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human lifter single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from NIPO at fitp.wipo.int/pub/published_pot_sequences

Length 47;

DB 4;

Score 48.5; DI Pred. No. 6.6;

41.1%;

Query Match Best Local Similarity

Sequence 47 AA;

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Chen W, Rank DR;

Hanzel DK,

Penn SG,

WPI; 2002-114183/15

(MOLE-) MOLECULAR DYNAMICS INC

2000GB-00024263

2000US-0207456P 2000US-00608408 2000US-00632366. 2000US-0234687P. 2000US-0236359P.

30-JUN-2000; 03-AUG-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

30-JAN-2001; 2001WO-US000665

WO200186003-A2.

15-NOV-2001

Homo sapiens

2000US-0180312P

04-FEB-2000; 26-MAY-2000; Claim 27; SEQ ID NO 30766; 634pp; English.

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microarrays having a probe with the exon, where a common pattern of microarrays having a probe with the exon, where a common pattern of the expression of the exons in the tissues and/or cell types indicates that the expression of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human ung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung diseases (LID), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Dulak syndrome, sarcoidosis, pulmonary lamonary alvolar proteinosis, thatioocytosis, lymphangioleiomyomicosis, pulmonary alvolar proteinosis, Asragener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp. wipo.int/pub/published_pct_sequences
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Sequence 47 AA;

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Gaps
                                    ij
     41.1%; Score 48.5; DB 5; Length 47; 60.0%; Pred. No. 6.6; ive 1; Mismatches 6; Indels
Query Match
Best Local Similarity 60.09
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1;

1 PRGAPMWMRWVCQMLETMFL 20 PRGAPNLGAWVLOCLE-IFL 31 13 à

AAY56647 RESULT

AAY56647;

AAY56647 standard; protein; 96 AA

Partial peptide fragment of chimpanzee VH cDNA clone 41-9.

(first entry)

15-FEB-2000

Complementarity determining region; antibody; primate; immunogenicity; old World ape; Old World monkey; antigen-binding affinity.

Pan troglodytes

WO9955369-A1

04~NOV-1999.

99WO-US009131. 28-APR-1999; (SMIK) SMITHKLINE BEECHAM CORP.

98US-0083367P.

28-APR-1998;

raylor AH;

WPI; 2000-023265/02. N-PSDB; AAZ39315 Antibodies containing donor complementarity determining regions and non-numan primate acceptor frameworks, having reduced immunogenicity in humans.

Claim 20; Page 55; 123pp; English.

The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspectific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigenspecific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated

Sequence 98 AA;

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The invention relates to an isolated lung specific polypeptide comprising an amino acid sequence 60% identical to a sequence chosen from 61 sequences such as 68, 63, 569, 51, 105, 711, 49 or 77 amino acids, or an amino acid sequence encoded by a nucleic acid molecule comprising a sequence chosen from 81 sequences such as 463, 554, 1074, 1277, 676, 524, 258 or 4106 bp given in the specification. The isolated polypeptide and its encoding polypurcleotide are useful for diagnosing and monitoring the presence and metastases of lung cancer in a patient, by determining an amount of the polypeptide or polynucleotide in a sample of a patient, and comparing it to the amount of lung specific marker in a normal control, where a difference in the amount of the nucleic acid or the polypeptide in the sample compared to that of normal control is associated with presence of lung cancer. The polypeptide and polynucleotide are useful as components in databases useful for search analyses and in sequence analysis algorithms. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for search analyses and in sequence analysis algorithms. The polymucleotide is useful for producing transgenic animals and cells and also in gene therapy. This sequence represents a lung-specific amino acid sequence relating to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic, lung specific protein, metastasis, lung cancer, gene therapy, transgenic animal, analysis algorithm; lung.
in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lung specific polypeptides useful for detecting, diagnosing, monitoring, treating, staging and predicting cancers in humans with cancer and non-
                                                                                                                                                      Gaps
                                                                                                                                                    ·.
                                                                                                             Length 96,
                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung-specific amino acid sequence SEQ ID No 107.
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                                                                                                             Score 48; DB 3; Pred. No. 16; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 210; 228pp; English.
                                                                                                                                                                                                                                                                                                                          AAO21796 standard; protein; 98 AA.
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20-NOV-2000; 2000US-0252055P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-2001; 2001WO-US050687
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                                                                                                             Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2002 (first entry)
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                                                                            Sequence 96 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                               AA021796;
                                          antibody
                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                          AA021796
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RESULT 11

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The invention relates to isolated polymoticolide (ii) and polypeptide (iii) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polymoticotides are also used in diagnostics as expressed sequence tags for identifying expressed control is useful in gene therapy techniques to restore normal activity of (II) is useful in gene tags for identifying expressed control in its useful in gene tags states involving (II). (I) is activity of (II) or to treat disease states involving (II). (II) is colypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in the activity. The polypeptide and polymotleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the vival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                     Human; chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.8%; Score 47; DB 4; Length 318; 44.4%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 45366; 103pp; English.
                                            Novel human diagnostic protein #14998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO83694 standard; protein; 421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PRGAPMWMRWVCQMLETM 18
                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS79194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 318 AA;
                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                     23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT,
                                                                                                                                                                                                                                 11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human specific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate projecins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -uou
                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity determining region; antibody; primate; immunogenicity; Old World ape; Old World monkey; antigen-binding affinity.
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies containing donor complementarity determining regions and human primate acceptor frameworks, having reduced immunogenicity in
                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.7%; Score 48; DB 3; Length 140; 87.5%; Pred. No. 23; 1; Indels iive 0; Mismatches 1; Indels
                       Length 98;
                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of chimpanzee VH cDNA clone 41-9.
                   Score 48; DB 5;
Pred. No. 16;
3; Mismatches
                                                                                                                                                                                                                                              AAY56712 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 46; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG15007 standard; protein; 318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                    1 PRGAPMWMRWVCQMLET 17
                                                                                                                                            PGGAHLWFFWLCDRVTT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0083367P.
                   40.7%;
ilarity 41.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.55,
                                                                                                                                                                                                                                                                                                                             (first entry)
Query Match
Best Local Similarity
'.hec 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WINGWVCOM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-023265/02.
N-PSDB; AAZ39315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09955369-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1998;
                                                                                                                                                                                                                                                                                                                             15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raylor AH;
                                                                                                                                                                                                                                                                                      AAY56712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody
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Gaps

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(first entry)

29-JUL-2004

ABG15007

RESULT 12

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ABG15007

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain acaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of [II]. The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of [I] is useful in gene therapy techniques to restore normal activity of [II] or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a colypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and [II] are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and cand sequences. ABGOGOIO-ABGIGGTY represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the electronic format directly from WIPO at the electronic format directly from WIPO at the construction of mutations and colectronic format directly from WIPO at the sequence of the construction of mutation of mutations and producted and
                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; vaccine; human; endometrial specific genes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human endometrial specific protein, SEQ ID NO 600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endometrial specific protein; endometrial cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 PRGGAXAWMRDRASIGADPVWLCPSLPSSFL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- WVCQMLETMFL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.4%; Score 46.5; D
38.7%; Pred. No. 91;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 38704; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE72560 standard; protein; 102 AA
                                                     30-MAR-2001; 2001WO-US008631.
                                                                                                           2000US-00540217.
2000US-00649167.
                                                                                                                                                                                                                                                Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2004 (first entry)
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                                                                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PR-GAPMWMR-
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Best Local Similarity
                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS72532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003060081-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity.
                                                                                                        31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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     11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE72560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE72560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to Pseudomonas aeruginosa polypeptides and the polypucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular tragets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P aeruginosa mucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                     Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy, forensic, food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 32440; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deloughery C,
Pseudomonas aeruginosa polypeptide #15869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #8336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG08345 standard; protein; 336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segdata.uspto.gov/seguence.html
                                                                                                                                                                                                                                                                       99US-00252991.
                                                                                                                                                                                                                                                                                                                          98US-0074788P.
                                                                                                                                                                                                                                                                                                                                                       98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nolling J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 PRGRPFWSKW 218
                                                                                                      Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PRGAPMWMRW 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-615309/58
N-PSDB; ABD17265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                           US6551795-B1
                                                                                                                                                                                                                                                                                                                          18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                       27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                 22-APR-2003
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5,

Gaps

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ABG08345

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4; Length 336; Indels

DB

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The invention comprises the amino acid and DNA sequences of human endometrial specific genes and proteins. The DNA and protein sequences of the invention are useful for diagnosing, imaging and treating a patient with endometrial cancer. The present amino acid sequence represents a human endometrial specific protein of the invention.
                                                                                                                                                         Nucleic acid molecules and polypeptides useful for diagnosing and treating endometrial cancer and non-cancerous disease states in endometrial.
                                                                                                                                                                                                                       Claim 12; SEQ ID NO 600; 824pp; English.
 23-DEC-2002; 2002WO-US041612.
                                 21-DEC-2001; 2001US-0342756P.
                                                               (DIAD-) DIADEXUS INC.
                                                                                                                           WPI; 2003-577666/54.
                                                                                               Liu C;
                                                                                            Sun Y,
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Query Match
Best Local Similarity 50.0%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 2; Indels 2 RGAPMWMR----WVCQ 13 ||||:| RGAPVWPERDTLWLCQ 80 ð g

Sequence 102 AA;

Search completed: October 26, 2004, 06:45:13 Job time : 89.5 secs

1,

4; Gaps

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October 26, 2004, 06:45:25; Search time 64.25 Seconds (without alignments) 100.781 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1364641 segs, 323758627 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    using sw model
                                                                                                                                                                                                                                                                                                                                                                                                      1 PRGAPMWMRWVCQMLETMFL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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118
                                                                                                                                - protein search,
                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                       OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 3, Appli	Sequence 22, Appl	Sequence 4, Appli	Sequence 23, Appl	Sequence 60423, A	Sequence 171, App	Sequence 8240, Ap	Sequence 199829,	Sequence 18537, A	Sequence 175423,	Seguence 38656, A	Seguence 15, Appl	Sequence 107, App
SUMMARIES	e	US-10-066-965A-3	US-10-066-965A-22	US-10-066-965A-4	US-10-066-965A-23	US-10-425-114-60423	US-09-771-161A-171	US-10-156-761-8240	US-10-437-963-199829	US-10-369-493-18537	S US-10-437-963-175423	US-09-864-761-38656	US-09-905-243-15	US-10-034-934-107
		14	14	14	14	15	0	14	16	14	16	6	6	14
	% Query Match Length DB	20	20	20	20	173	123	307	87	429	1451	47	96	98
	% Query Match	100.0	100.0	81.4	81.4	47.5	42.8	42.8	42.4	41.5	41.5	41.1	40.7	40.7
	Score	118	118	96	96	26	50.5	50.5	20	49	49	48.5	48	48
	Result No.	н	7	m	4	2	9	7	80	Q	10	11	12	13

Sequence 204224,	e 10442	۵	۵	۵		Sequence 51232, A		Sequence 169363,	Sequence 167292,		Sequence 188631,	ednence	Sequence 127057,	a)	Sequence 184426,	a)					Sequence 2, Appli	equence	equence		equence	ednence	ω	equence	Sequence 314, App	(D)	Sequence 314, App	
US-10-424-599-204224	-156-761-1	-437-963-1337	0-289-762-	0-312-273	-802-741A-	.0-282-122A	10-437-963-	.0-424-599-	.0-437-963-	10-425-114-	63-18	10-437-963-	10-437-963-1	10-437-963-16	-10-424-599-18	10-108-2	-10-424-599-	796-25	882-87	184-648-	-296-606-	-106-534	0-006-867-1	US-10-052-586-314	-063-5	0-063-551-1	10-174-5	-10-176-7	10-175-737-31	10-063-616-1	-10-174-581-31	!
15	14	16	15	15	6	15	16	15	16	15	16	16	16	16	15	15	15			4	ഹ	ന	ന	3	ന	m	14		14	14	14	
63	260	358	196	476	584	629	37	211	267	356	583	913	116	155	74	308	337	368	376	376	376	413	414	414	414	414	414	414	414	414	414	
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4.7	47	47	46	46	46		45	45	4.5	45	45	45		4.	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

APPLICANT: COLAS, PIERRE
APPLICANT: COLAS, PIERRE
APPLICANT: COLAS, PIERRE
APPLICANT: COLAS, PIERRE
APPLICANT: COLES, PIERRE
APPLICANT: COLES, PIERRE
APPLICANT: COLES, PIERRE
APPLICANT: COLEN, BARK A.
ITILE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REPERBNCE: BGYP 3. 0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide 1./ Length 20; Query Match 100.0%; Score 118; DB 14; Best Local Similarity 100.0%; Pred. No. 4.8e-10; Matches 20; Conservative 0; Mismatches 0; ORGANISM: Artificial Sequence US-10-066-965A-3 US-10-066-965A-3 LENGTH: 20 TYPE: PRT FEATURE

qq

0;

Gaps

0

Indels

RESULT 2 US-10-066-965A-22 Sequence 22, Application US/10066965A Publication No. US20030143626A1

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US-10-066-965A-23
                                                                            TYPE: PRT
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              APPLICANT: COLAS, PIERRE
APPLICANT: COLAS, PIERRE
APPLICANT: COLAS, ROGER
APPLICANT: COLES, BARAK A.

TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: EGYP 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 22
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COLAS, PIERRE
APPLICANT: BRENT, ROGER
APPLICANT: GOTEN, BARAK A.
TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: EGYP 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 33
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APPLICANT: COLAS, PIERRE
APPLICANT: COHEN, BREAK A.
TITLE OF INVENTION: TRAGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: EGYP 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide
US-10-066-965A-4
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 118; DB 14; Best Local Similarity 100.0%; Pred. No. 4.8e-10; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 23, Application US/10066965A
; Publication No. US20030143626A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10066965A
Publication No. US20030143626A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PRGAPMWMRWVCQMLETMFL 20
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                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
GENERAL INFORMATION:
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US-10-066-965A-22
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US-10-066-965A-23
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LENGTH: 20
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APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Tark OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 60423
                                                                                                                                                                                                                                                                                         0;
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                                                                                                                    FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                         ..
0
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                                                                                                                                                                                                                                     Score 96; DB 14; Length 20;
Pred. No. 7e-07;
                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
; OTHER INFORMATION: Clone ID: LIB3592-081-All_FLI.pep
US-10-425-114-60423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-771-161A-171
Sequence 171, Application US/09771161A
Sequence 171, Application US/09771161A
Sequence 171, Application US/09771161A
GENERAL INFORMATION:
TITLE OF INVENTION: VARIANTS OF ENCTEIN KINASES
FILE REPERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 13676
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATENTING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SEQ ID NO 171
LENGTH: 123
                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60423, Application US/10425114
Publication No. US20040034888A1
CENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                   1 PRGAPMWMRWVCQMLETMFL 20
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Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.5%;
                                                                                           ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 20
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
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US-10-425-114-60423
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Gren, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US, 0310/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICANION NUMBER: US, 60/360, 039
PRIOR FILING DATE: 2002-02-21
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61;
                                                                Length 87;
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                                                                                                       Indels
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95359C.1.pep
US-10-437-963-199829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT4530_7326C.1.pep
                                                              Score 50; DB 16;
Pred. No. 11;
6; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 175423, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bubacuk, Brad
; APPLICANT: Bubacuk, Brad
; APPLICANT: Bubacuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 41.2%; Pred. No.
Matches 7; Conservative 3; Mismatc
                                                                                                                                                                                                                                                                                               Sequence 18537, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 GLSMWMTWKCAVMDLPF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GAPMWMRWVCQMLETMF 19
                                                                                                                                                     3 GAPMWIRWVCQMLETMF 19
                                                                                                                                                                                              83
                                                                   42.4%;
                                                                                                                                                                               69 GAPVW--WTCELVEVVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 18537
                                                      TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-437-963-175423
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US-10-437-963-175423
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LENGTH: 1451
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                   Length 123;
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                                                                                                                                          Indels
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                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11arity 56.2%; Score 50.5; Dilarity 56.2%; Pred. No. 28; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: IKEDA, HAROO
APPLICANT: IKEDA, HAROO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, WASAHIRA
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8240
SEQ ID NOS: 15109
                                                                                                 11arity 42.9%; Score 50.5; I clarity 42.9%; Pred. No. 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 199829, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                Sequence 8240, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                     ---APMWMRWVC 12
                                                                                                                                                                                                                            79 PRGHKISDYFETAPLWFRWQC 99
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Boukharov, Andrey A.
Barbazuk, Brad
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ORGANISM: Oryza sativa
                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                           Best Local Similarity
Matches 9; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                     Query Match
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APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0245
CURRENT APPLICATION NUMBER: 80/243,461
PRIOR APPLICATION NUMBER: 60/243,461
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR PLILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                            Gaps
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                         OTHER INFORMATION: EST_HUMAN HIT: BF241410.1, EVALUE 6.00e-01
                                                                                                                             Length 47;
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Sequence 15, Application US/09905243

Sequence 15, Application US/09905243

Betent No. US20020062009A1

GENERAL INFORMATION:

APPLICANT: Taylor, Alexander H

TITLE OF INVENTION: Immunogenicity

TITLE OF INVENTION: Immunogenicity

FILE REFERENCE: PS0770

CURRENT APPLICATION NUMBER: US/09/905,243

CURRENT APPLICATION NUMBER: US/09/905,243

FRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 97

SEQ ID NO 15

SEQ ID NO 15

LENGTH: 96
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87.5%; Pred. No. 23;
tive 0; Mismatches
                                                                                                                          DB
                                                                                                             Query Match
41.1%; Score 48.5; Dest Local Similarity 60.0%; Pred. No. 10; Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107, Application US/10034934
; Publication No. US20030068624A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                        1 PRGAPMWMRWVCQMLETMFL 20
                                                                                                                                                                                                                                                                                 13 PRGAPNLGAWVLQCLE-IFL 31
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
US-09-905-243-15
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OTHER INFORMATION: CDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 WMRWVCQM 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: DOMAIN
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                                  ; OLDER IN 138656
US-09-864-761-38656
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; Sequence 38656, Application US/09864761
; Sequence 38656, Application US/09864761
; Sequence 38656, Application US/09864761
; APPLICANT: Fank, David R.
; APPLICANT: Hanzel, David R.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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                                                  Gaps
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                                               Indels
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EXPRESSED IN LUNG, SIGNAL = 1.5
EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
EXPRESSED IN BRAIN, SIGNAL = 1.4
EXPRESSED IN BONE MARROW, SIGNAL = 1.3
EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
EXPRESSED IN HEART, SIGNAL = 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HILLE DEFENDER: AGNE EXPRESSION ANALYSIS BY MICRO;
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-08-36
PRIOR PILING DATE: 2000-09-37
PRIOR PELING DATE: 2000-09-37
PRIOR PELING DATE: 2000-10-39
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-
Best Local Similarity 41.2%; Pred. No. 1.8e+02; Matches 7; Conservative 3; Mismatches 7_i
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OTHER INFORMATION: EXPRESSED IN PLACENY
OTHER INFORMATION: EXPRESSED IN LUNG, &
OTHER INFORMATION: EXPRESSED IN BETAL I
OTHER INFORMATION: EXPRESSED IN BRAIN,
OTHER INFORMATION: EXPRESSED IN BONE MA
OTHER INFORMATION: EXPRESSED IN BOULT I
OTHER INFORMATION: EXPRESSED IN HEART,
                                                                                                                                                         908 GLPLWCLWALQMLRSWY 924
                                                                                              3 GAPMWARWVCQMLETMF 19
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Karola Thomas J
APPLICANT: APPLICANT: About K
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 204224
LIENGTH: 63
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                                                                                                               Query Match 40.7%; Score 48; DB 14; Length 98; Best Local Similarity 41.2%; Pred. No. 23; Matches 7; Conservative 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_26441C.1.pep
US-10-424-599-204224
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Pred. No. 22;
2; Mismatches 4
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Sequence 10442, Application US/10156761

Sequence 10442, Application US/10156761

GENERAL INFORMATION:
APPLICANT: EREDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHORE, 190-1000

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 10442
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80 PGGAHLWFFWLCDRVTT 96
                                                                                                                                                                                                              1 PRGAPMWMRWVCQMLET 17
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                   TYPE: PRT
CORGANISM: Homo sapiens
US-10-034-934-107
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Best Local Similarity
Matches 6; Conserva
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LENGTH: 98
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Score 47; DB 14; Length 260;
Pred. No. 77;
0; Mismatches 4; Indels
 39.8%;
                         8; Conservative
Query Match
Best Local Similarity
Matches 8; Conserv
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1 PRGAPMWMRWVC 12

68 PRGAPRWPAGVC 79

Search completed: October 26, 2004, 07:10:19 Job time : 65.25 secs

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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/037,248
FILING DATE: March 26, 1993
ATTORNEY, AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 63475/12
TELECOMONICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELERX: (212) 286-0854 or 286-0082
TELERX: TWX 710-581-4766
INFORMATION POR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: cDNA to mRNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: doi
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                              RESULT 1
US-09-070-356-7
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Sequence 20438, A
Sequence 23440, A
Sequence 134, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 45700, A
Sequence 5500, A
Sequence 5500, A
Sequence 5500, A
Sequence 5700, A
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53062, A
4, Appli
38878, A
54095, A
2, Appli
3, Appli
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                                                                                  October 26, 2004, 06:20:00 ; Search time 22 Seconds (without alignments) 60.289 Million cell updates/sec
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Sequence 5
Sequence 4
Sequence 3
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Sequence 4
Sequence 1
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Sequence
Sequence
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1: /Ggn2_6/prodata1/laa/5A_COMB.pep:*
/Ggn2_6/prodata1/laa/5B_COMB.pep:*
3: /Ggn2_6/prodata1/laa/6A_COMB.pep:*
4: /Ggn2_6/prodata1/laa/6B_COMB.pep:*
5: /Ggn2_6/prodata1/laa/PCTUS_COMB.pep:*
6: /Ggn2_6/prodata1/laa/PCTUS_COMB.pep:*
6: /Ggn2_6/prodata1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-352-5500
US-09-270-767-38667
US-09-270-767-53884
US-08-860-820-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-32440
US-08-545-803A-134
US-09-198-452A-454
US-08-987-466-4
US-08-240-359-4
US-09-270-767-45700
US-08-991-677-6
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US-08-525-539A-24
US-09-270-767-37845
US-09-270-767-53062
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-09-248-796A-20438
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US-09-270-767-38878
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US-09-614-912-144
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                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-904-871-3
                                                                                                                                                                                                                                              478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                           118
1 PRGAPMWMRWVCQMLETMFL 20
                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                             US-10-066-965A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                          Run on:
                                                                                                                                                Title:
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double

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Sequence 18260, A Sequence 7, Appli Sequence 105, Appli Sequence 106, App Sequence 109, App Sequence 111, App Sequence 112, App Sequence 113, App Sequence 115, App Sequence 115, App Sequence 115, App Sequence 116, App Sequence 1117, App Sequence 1118, App
                                                 52838, A
18260, A
7, Appli
8, Appli
Sequence
Sequence
Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,356
                     US-09-270-767-37621
US-09-270-767-37621
US-09-248-796A-18260
US-09-355-925-7
US-09-355-921-105
US-09-269-921-106
US-09-269-921-109
US-09-269-921-110
US-09-269-921-111
US-09-269-921-111
US-09-269-921-111
US-09-269-921-112
US-09-269-921-113
US-09-269-921-113
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Patent No. 6226631

GENERAL INFORMATION:
APPLICANT: Jack Goldstein
TITLE OF INVENTION: Recombinant a-N-
TITLE OF INVENTION: Brayme and cDNA Encoding
TITLE OF INVENTION: Brayme and cDNA Encoding
TITLE OF INVENTION: Said Enzyme
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Amater, Rothstein & Ebenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Amster, Rothstein & Ebenstein STREET: 90 Park Avenue CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-269-921-115
US-09-269-921-116
US-09-269-921-117
US-09-269-921-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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ORIGINAL SOURCE:

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32440
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Sequence 134, Application US/08545809A

Sequence 134, Application US/08545809A

GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku

APPLICANT: Matsuda, Fumihiko

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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MEDIUM TYPE: Diskette:
COMPUTER: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                    ; Sequence 32440, Application US/09252991A; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 116 amino acids
amino acid
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INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 PRGRPFWSKW 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PRGAPMWMRW 10
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Best Local Similarity
                                                                                     US-09-252-991A-32440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-32440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: TO/196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Aspergillus niger a-galactosidase LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: den Herder et al
TITLE: Cloning and Expression of a Member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE: of the Aspergillus niger Gene Family IITLE: Encoding a-Galactosidase JOURNAL: Molecular and General Genetics PAGES: 404-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.1%; Pred. No. 9;
Matches 8; Conservative 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 PHNWPMWLKWWYTFIISMFV 123
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ORGANISM: Aspergillis niger
                                                                                     DEVELOPENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CRELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: library
POSITION IN GENOME: unknown
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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ORGANISM: Candida albicans
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                              STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
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TITLE:
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Pred. No. 48;
                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fisher, Doug
APPLICANT: Streeter, Dave
APPLICANT: Streeter, Dave
TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 3;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PSESEO for Windows Version 2.0 SOFTWARE: PSESEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,359
FILING DATE:
                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0442 US
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APPLICATION NUMBER: 08/987,466
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09240359
Patent No. 6255456
            TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEPAX: 650-845-0466
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.0%;
43.8%;
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414 PLYKRWVALLMEEFFL 429
                                                                                                                                                                                                                                                                                       39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 584 amino acid
TYPE: amino acid
STRANDEDNESS: single
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    5 PMWMRWVCOMLETMFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 3174 Porter Dr
Palo Alto
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                          STREET TOPOLOGY: LILEGALINMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBa
CLONE: 829179
                                                                                                                                                                                                           ; LIBRARY: GenB.
; CLONE: 829179
US-08-987-466-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-359-4
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US-09-198-452A-454
US-09-198-452A-454
Sequence 454, Application US/09198452A
Patent No. 655224
GENERAL INFORMATION:
APPLICANT: GITIFais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE FERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 454
LENGTH: 196
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                                                                                                                          Gaps
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                                                                                  39.0%; Score 46; DB 3; Length 116; 70.0%; Pred. No. 9.1;
                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08987466
Sequence 4, Application US/08987466
Ratent No. 5922595
GENERAL INFORMATION:
APPLICANT: Fisher, Douglas A.
APPLICANT: Gooding, Doug
APPLICANT: Streeter, Dave
TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastERG for Windows Version 2.0 SOFTWARE: FastERG for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,466
FILLING DATE: Filed Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNAY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PMWMRWVCQMLE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
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                                                                                        Query Match 39.0
Best Local Similarity 70.0
Matches 7; Conservative
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COMPUTER READABLE FORM:
            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-134
                                                                                                                                                                   7 WMRWVCQMLE 16
                                                                                                                                                                                                       51 WMHWVCQAPE 60
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Matches 5; Conserv
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Conservative

7;

Matches

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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38667, Application US/09270767
Sequence 38667, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION
APPLICANT: Homburger et al.
TILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: FILE REFERENCE: FILE REFERENCE: T326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
EBNGTH: 91
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Pred. No. 2.7e+02;
2; Mismatches 1; Indels
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36.4%; Score 43; DB 4; Length 133
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 7; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 4; Length 91;
Pred. No. 29;
2; Mismatches 0; Indels
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    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,789
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24340
LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5500, Application US/09328352 Patent No. 6562958
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                                                                                                                                                                                                                TYPE: PRT CRGANISM: Pseudomonas aeruginosa US-09-252-991A-24340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Acinetobacter baumannii
US-09-328-352-5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-38667
                                                                                                                                                                                                                                                                                                    36.48;
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                               6; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-09-270-767-38667
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US-09-328-352-5500
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45700
LENGTH: 115
        Gaps
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APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Carraway, Daniel T
APPLICANT: Carraway, Daniel T
TALE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1996-12-16
BARLIER FILING DATE: 1996-12-16
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH. 368
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46.2%; Pred. No. 13;
1ve 1; Mismatches 6; Indels
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    Indels
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41.7%; Pred. No. 60;
tive 5; Mismatches
Mismatches
                                                                                                                                   RESULT 8
US-09-270-767-45700
; Sequence 45700, Application US/09270767
; Patent No. 6703491
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Patent No. 6551795
GENERAL INFORMATION:
FAPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AND TITLE OF INVENTION: AERUGINOSA FOR DIAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ' Sequence 6, Application US/08991677A
' Patent No. 6252135
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Drosophila melanogaster
US-09-270-767-45700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Liquidambar styraciflua
US-08-991-677-6
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                                                                             414 PLYKRWVALLMEEFFL
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Best Local Similarity 46.2
Matches 6; Conservative
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US-09-252-991A-24340
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US-08-991-677-6
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; MOLECULE TYPE: protein US-08-860-820-2
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Patent No. 6245967
GENERAL INFORMATION:
APPLICANT: Somewald, Uwe
APPLICANT: Kossmann, Jens
APPLICANT: Bowien, Botho
TITLE OF INVENTION: PROCESS AND DNA MOLECULES FOR INCREASING
TITLE OF INVENTION: THE PHOTOSYNTHESIS RATE IN PLANTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               35.6%; Score 42; DB 4; Length 91; 75.0%; Pred. No. 29; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC COMPATIBLE
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,820
FILING DATE: 04-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19502053.7
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1251 Avenue of the Americas CITY: New York STATE: New York STATE: New York ZIP: 1020
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                        US-09-270-767-53884
; Sequence 53884, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT CRGANISM: Drosophila melanogaster US-09-270-767-53884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 PRGAPVWV 72
               ||||||:|:
PRGAPVWV 72
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US-08-860-820-2
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Sequence 170, Application US/08311731A

Sequence 170, Application US/08311731A

Patent No. 6.883266

GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LABRAE FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPENDENCE ADDRESS:
ADDRESSEE: WOLF, CREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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Pred. No. 1.4e+02;
0; Mismatches 3; Indels
            35.6%; Score 42; DB 3; Length 364; 46.7%; Pred. No. 1.2e+02; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATION SYSTEM: FOLLOWING TO VERSION #1.25
SOFTWARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATE: DUMRER: 31,616
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: October 26, 2004, 06:47:57 Job time : 23 secs
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palaca
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ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 ATLANTIC AVENUE
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66.7%;
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Matches 6; Conservative
Ouery Match
Best Local Similarity 46.7.
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RGAPMWMRW 10
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                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-311-731A-170
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 26, 2004, 06:19:49; Search time 17 Seconds (without alignments) 113.196 Million cell updates/sec

US-10-066-965A-4 115 1 PRGAPMWLRCVCQMLETKFL 20 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	~	ydrog	hypothetical prote	•	titin, cardiac mus		phosphocarrier pro	probable transcrip		hypothetical prote	alpha-galactosidas	NGFI-A-binding pro	caspase-related pr	cell wall alpha-gl	conserved hypothet	-di	phytochrome - Mars		probable GABA perm	probable protein k	protochlorophyllid	N-acetylglucosamin	N-acetylglucosamin		ŭ	-н	hypothetical prote	-like	protein-tyrosine k
dī	T4380		T2950		I38344		B8206		H8	S	S	I59	T43		695	H95	ςΩ		Ξ		A36904	ם	JC7351	щ	H			T086	
DB	~	N	7	7	Н	7	7	~1	N	7	7	7	~	N	C3	7	7	7	~	7							7	7	7
Length	1044	773	413	1483	26926	622	92	299	322	542	545	570	826	2410	122	165	190				466	484	486	499	618	618	169	8	992
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Score	50	47	44	44	44	42.5	42	42	42	42	42	42	42	42	41	41	41	41	41	41	41	41	41	41	41	41	41	41	4.
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RESULT 2
JUD135
JUD135
JUD135
JUD135
JUD136
JUD136
JUD136
JUD137

protein-tyrosine k	FICS PIOCELL " WOL	phytocuroune / proc	genome polyprotein	nonstructural poly	replicase polyprot	hypothetical prote	hypothetical prote	conserved hypothet	conserved hypothet	hypothetical prote	membrane associate	pyruvate dehydroge	transketolase NMB1	transketolase (EC	homeobox protein (
A36873	S18827	827396	GNNY89	MNWVRA	T03725	T51913	T24116	AI1506	AI1147	T37509	B97095	H75540	B81082	A81862	D96829
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993	1000	1303	2164	2479	1759	253	318	389	390	432	452	617	629	629	745
35.7	35.7	35.7	35.7	35.7	35.2	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8
41	41	41	41	41	40.5	40	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	3.7	3.8	6 6	40	41	42	43	44	45

ALIGNMENTS

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A, Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB
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A,Cross-references: UNIPROT:Q10466; EMBL:X90568; NID:g1017424; PID:g1017425
A,Cross-references: UNIPROT:Q10466; EMBL:X90568; NID:g1017424; PID:g1017425
B,Musco, G, Tziatzios, C, Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
A,Title: Dissecting titin into its structural motifs: identification of an alpha-helix m A,Reference number: 138345; MUID:95119041; PMID:7819249
A,Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Mossives: P, 22278-22431, R', 22433-22448, 'G', 22450-22453, 'Q', 22455-22480, 'TR', 22483-2
A;Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
B;Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
J. Mol. Biol. 256, 556-563, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R, Gautel, M.; Leonard, K.; Labeit, S.
EMBO J. 12, 3827-3834, 1993
A;Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differentiats
A;Reference number: S37393; MUID:94008990; PMID:8404852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Molecule type: mRNA
A. Residues: 1977-2014 cMUS>
A. Residues: 1977-2014 cMUS>
A. Residues: 1977-2014 cMUS>
A. Residues: 1977-2014 cMUS>
A. A. Cross-references: EMBI:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580
A. Molec: conformation and properties are reported for a synthetic peptide corresponding in R. Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A. Trile: Towards a molecular understanding of titin.
A. Trile: Towards a molecular understanding of titin.
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                                                                                                                                                                                    Litin, cardiac muscle [validated] - human
N'Alternate names: connectin
N'Alternate names: connectin
N'Alternate names: connectin
N'Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 09-Jul-2004
C'Accession: 138344; 138345; S20898; S20899; S63665; S37393
R'Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A,Tille: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A,Reference number: A57430; MUID:96026330; PMID:7569978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A66201; PDB:1NCT
A;Contents: annotation; conformation by (1)H-NMR, residues 'S',26059-26155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 13597-14200,'I',14202-14696 <LAB2>
A;Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
A;Accession: S20897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3>
A;Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues 5253-5341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Improta, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A;Reference number: A66736; PDB:1TIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents: annotation; conformation by (1)H-NMR, residues R; Ffuhl, M.; Pastore, A. Submitted to the Brookhaven Protein Data Bank, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 26729-26825 <KOL>
A,Cross-references: EMBL:X92412; NID:g1236761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown
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A; Residues: 26831-26926 <GAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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                                                     A; Residues: 1-773 <TAM>
A; Residues: 1-773 <TAM>
A; Residues: UNIPROT: P17201
C; Comment: This enzyme is a membrane-bound protein.
C; Comment: Alcohol and aldehyde dehydrogenases are two enzymes in Acetobacter species wh C; Superfamily: isoquinoline 1-oxidoreductase beta subunit C; Keywords: oxidoreductase
C; Keywords: oxidoreductase
F; 1-44/Domain: signal sequence #status predicted <SIG>F; 1-44/Domain: aldehyde dehydrogenase #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515/2; 538/1; 555/3; 782/1; 979/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F43H9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T29505
C;Accession: T29505
R;Wu, X.; Le, T.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid F43H9.
A;Reference number: Z20629
A;Reference number: Z20629
A;Reference number: Z20629
A;Reference number: T29505
A;Reference: T29505
A;Residues: 1-413 < WUX>
A;Residues: 1-413 < WUX>
A;Residues: 1-413 < WUX>
A;Residues: 1-413 < WUX>
A;Residues: 3.1,13 < WUX>
A;Experimental source: strain Bristol N2
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Introns: 32/1; 138/2; 206/3; 292/1; 379/1
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942839
116G12: 5 protein - Caenorhabditis elegans
C;8pecies: Caenorhabditis elegans
C;8pecies: Caenorhabditis elegans
C;8pecies: Caenorhabditis elegans
C;Bate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42839
B;Thomas, K.
Submitted to the EMBL Data Library, February 1994
A;Accession: S42837
A;Accession: S42839
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1483 CHG>A;Accession: NATH,A467461
A;Residues: 1-1483 CHG>A;Accession: NATH,A467461
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 2; Length 773;
Pred. No. 17;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.3%; Score 44; DB 2; Length 413; 46.2%; Pred, No. 28;
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C;Superfamily: Caenorhabditis elegans T16G12.5 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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Similarity 61.5%;
8; Conservative
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A; Molecule type: DNA
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Best Local Similarity
Matches 8; Conserv
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Matches 6; Conserv
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Query Match

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Query Match Best Loc Matches m

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A; Cross-references: UNIPROT: Q50900; EMBL: Z21955; NID: 9577589; PIDN: CAA79965.1; PID: 957755

A; Cross-references: UNIPROT: Q50900; EMBL: Z21955; NID: 9577589; PIDN: CAA79965.1; PID: 957755

Bur. J. Biochem. 233, 238-248, 1995

A; Title: A cluster of structural and regulatory genes for light-induced carotenogenesis in A; Feference number: S67950; MUID: 96061955; PMID: 7588751

A; Accession: S67958

A; Status: nucleic acid sequence not shown
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Nature 409, 1007-1011, 2001
A, Puthors: Nutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; Litle: Massive gene decay in the leprosy bacillus.
A, Rithermore number: A86909; MUID:21128732; PMID:11234002
A, Accession: H87131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable transcription regulator (carotenoid gene cluster orf 11) - Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Myxococcus xanthus
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                             Length 92;
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Pred. No. 44;
                                                                                             2;
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36.5%; Score 42; DB
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches
                                                                                         Score 42; DB 2
Pred. No. 15;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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58.3%;
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C, Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                           Conservative
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                                                                   Query Match
Best Local Similarity
7, Conserva
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Best Local Similarity
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A; Residues: 1-322 <STO>
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A; Residues: 1-299 <BOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 7-68 <BOW>
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                                     A; Map position: 1
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A; Gene: VC2533
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R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Dougen, G.;
il, M.; Rutherford, A.M.; Chillingworth, T.; Cronin, J.; Stevens, R.M.; Davis, P.; Dougen, G.;
il, M.; Rutherford, A.W.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Fitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001, MUID:21470413; PMID:11586360
A;Accession: AG0001
A;Acc
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A;Gene: kup
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Accession: B82060 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82060 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82060 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82066
C;Accession: B8206
C;Accession: B8206
C;Accession: B82066
A;Accession: B82066
A;Accession: B82066
                                                                                                                                                                                                                                                                                                                                                                                                    tatus predicted
F;16780,16976,17579,17602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,18
,21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,248
F;26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphocarrier protein NPr VC2533 [imported] - Vibrio cholerae (strain N16961 serogroup
                                                                                                                                          A;Description: structural protein forming filaments in striated muscle (5,Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; pro C;Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glycd
                                                                                                                                                                                                                                                                     structural protein
124752-25008/Domain: protein kinase homology «KIN»
F;84 177,905,2276,2278,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068,
98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,7
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.2e+03;
3; Mismatches 7; Indels (
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Best Local Similarity 41.7%; Pred. No. 70;
Matches 10; Conservative 3; Mismatches
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A,Cross-references: GDB:127867; OMIM:188840
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Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                              A,Map position: 2q31-2q32
C,Function:
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A:Molecule type: DNA
A:Residues: 1-92 <HEI>
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Proc. Natl. Acad. Sci. U.S.A. 92, 6873-6877, 1995
A;Title: Identification of NAB1, a repressor of NGFI-A- and Krox20-mediated transcriptic A;Reference number: IS9402, MUID:95350172; PMID:7624335
A;Accession: IS9402
A;Accession: IS9402
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-570 <RES>
A;Cross-references: EMBL:U17253; NID:9915281; PIDN:AAC52236.1; PID:9915282
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A;Cross-references: UNIPROT:Q9Y055; EMBL:AF088288; NID:g4063373; PIDN:AAC98295.1; PID:g4
A;Accession: T43639
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C'Date: 21.Jan-2000 #sequence revision 21-Jan-2000 #text change 09-Jul-2004 C'Accession: T43731; T43435; T41740; T40920; T43003; T43746; T41143 R;Hochstenbach, F.; Klis, F.M.; van den Ende, H.; van Donselaar, E.; Peters, P.J.; Klausr Proc. Natl. Acad. Sci. U.S.A. 95, 9161-9166, 1998 A;Title: Identification of a putative alpha-glucan synthase essential for cell wall const A;Reference number: Z22653; MUID:98356128; PMID:9689051
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A)Cross-references: UNIPROT:Q9USK8; EMBL:AF061180; NID:g3414806; PIDN:AAC31430.1; PID:g3*<br/>
R;Katayama, S:, Dai, H.; Arellano, M.; Perez, P.; Toda, T.<br/>
submitted to the EMBL Data Library, October 1998<br/>
A;Description: Fission yeast alpha-glucan synthase Mok1 localizes closely with actin play<br/>
A;Reference number: Z22511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 273, 35109-35117, 1998
Affilte: Identification of multiple Caenorhabditis elegans caspases and their potential
A;Reference number: 222587; MUID:99074291; PMID:9857046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 564-826 <SH2>
A;Cross-references: EMBL:AF088289; NID:g4063375; PIDN:AAC98296.1; PID:g4063376
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43638; T43639
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75.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                       36.5%; Score 42; DB 2;
43.8%; Pred. No. 78;
tive 1; Mismatches
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Keywords: cysteine proteinase; hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PMWLRCVC 12
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Shaham, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
$23382
alphacatosidase (EC 3.2.1.22) precursor - Aspergillus niger
C;Bpecies: Aspergillus niger
C;Bate: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: 823582, 82563; $18851
A;Altle: cloning and expression of a member of the Aspergillus niger gene family encodin
A;Reference number: $23582; MUID:92318893; PMID:1320186
A;Accession: $23582
A;Accession: $23582
A;Accession: $25582; MUID:92318893; PMID:1320186
A;Accession: $25582
A;Accession: $25582
A;Accession: $25582
A;Accession: $25582
A;Accession: $25582
A;Accession: $2559
A;Accession: $2550
A;Accession
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                                                                                                                                                     hypothetical protein SPAC31A2.06 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
159402
159402
C. Pabinding protein NAB1 [imported] - rat
C. Species: Rattus norvegicus (Norway rat)
C. Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
C. Accession: I59402
R. Russo, M.W.; Sevetson, B.R.; Milbrandt, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 75;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|||:| | :|: |:
83 PKGAPNFLADVI,NLLKKKY 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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Best Local Similarity 42.1%;
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Best Local Similarity 42.1'
Matches 8; Conservative
271 QGAPDWMRC 279
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                                                                                          RESULT 10
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Gaps

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Length 122; Indels

5; DB .

5; Mismatches Score 41; Pred. No. 2

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: L122 *KLES
A;Rosatudes: L122 *KLES
A;Cross-references: UNIPROT:028021; GB:AE000948; GB:AE000782; NID:92689271; PIDN:AAB8898;
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF2263
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A62250; MulD:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      completed: October 26, 2004, 06:46:25
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 KGAPVSLSAIQKMLEREF
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Matches 8; Conserv
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A; Status: translated from GB/EMBL/DDBJ
A; Residues: 1392-2410 < VOL>
A; Residues: 1392-2410 < VOL>
A; Residues: 1392-2410 < VOL>
A; Cross references: EMBL:AL035218; NID:g4160576; PIDN:CAA22822.1; PID:g4160577; GSPDB:GN
A; Experimental source: strain 972h-; cosmid c1281
B; Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
B; Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
A; Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A; Reference number: Z17323; MUID:98162722; PMID:9501991
A; Rocession: T43003
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: T41740
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-255, Y', 257-1210 < LNN>
A,Residues: 1-255, Y', 257-1210 < LNN>
A,Residues: 10-255, Y', 257-1210 < LNN>
A,Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: EMBL:AL049472, NID:g4538675; PIDN:CAB39330.1; PID:g4538676; GSPDB:GN
A,Experimental source: strain 972h-; cosmid c17A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Function:
A;Description: involved in cell morphogenesis independently of the actin cytoskeleton;
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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A, Status: translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 2076-2410 cHGC2>
A, Cross-references: EMBL.AF063305; NID:g3387871; PIDN:AAC39519.1; PID:g3387872
A, Experimental source: strain 972
A, Experimental source: strain 972
A, Experimental source: strain 972
A, Efference number: Z21972
A, Reference number: Z21972
A, A, Ccossion: T41143
A, A, Cossion: translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1157-1465 cWOO>
A, Residues: 1157-1
                                                                                                                                                                                                                                        A;Residues: 1-1848, 'A',1850-2027,'C',2029-2410 <KAT>
A;Cross-references: EMBL:AB019183; NID:g3808057; PIDN:BAA34054.1; PID:g3808058
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D. submitted to the EMBL Data Library, June 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: D89202; NID:g1749611; PIDN: BAA13863.1; PID:g1749612 A; Cross-references: EMBL: D89202; NID:g1749611; PIDN: BAA13863.1; PID:g1749612 A; Experimental source: strain PR745 R; Hochstenbach, F.; Klausner, R.D. submitted to the EMBL Data Library, May 1998 A; Reference number: Z22659
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A; Residues: 2044-2410 < YOS>
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Matches 5; Conserv
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                                                                         A; Accession: T43435
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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 26, 2004, 06:09:56; Search time 93 Seconds (without alignments) 123.736 Million cell updates/sec Run on:

US-10-066-965A-4 115 1 PRGAPMWLRCVCQMLETKFL 20 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 2 2 4 2 4 2 4 5 6 6 6		-HC	1044	-	BUB1 SCHPO	1
W 4 N 6 V 8 V		C	579	7	Q7TSE3	
4106780		>	188	7	Q9FSA3	
N 0 V 0 0		0	773	Н	DHAQ ACEPO	acetoba
9 C 8 G			913	~	090 <u>x</u> B9	Q90xb9 gallus gall
V 80 0		40.0	307	N	Q70IN1	Q70inl pseudomonas
ω σ		40.0	307	~	CAE45100	0
6		40.0	773	~	030329	030329 acetobacter
		39.1	120	~	Q8FP46	Q8fp46 corynebacte
10	45		251	7	Q93HK1	Q93hk1 streptomyce
11	45	39.1	260	7	082J76	Q82j76 streptomyce
12	45		371	7	Q8BP03	
13	45	39:1	441	~	Q7RY30	0
14	45	39.1	486	ď	087032	_
15	45	39.1	663	7	Q8K0Q5	_
16	44	38.3	140	(7	Ф863Н0	 C
17	44	38.3	243	7	Q93FT4	
18	44	38.3	256	~	Q9FIV4	
19	44		348	7	Q91TR9	_
20	44	38.3	413	7	Q20377	7
21	44	8	485	Н	NAB1 MESAU	σ
22	44	38.3	1142	7	Q225 <u>2</u> 8	8 caenc
23	44	8	26926	0	Q10466	homo
24	44	8	26926	~	Q8WZB3	homod
25	44	38.3	34350	7	Q8WZ42	рошо
26		7.	Q,	7	Q6Z9Y3	ryz
27		7.	9	~	BAC98592	oryza
28	Э.	7.	σ	7	BAC99593	Bac99593 oryza sat
29	43.5	37.8	272	7	Q6NK48	Q6nk48 corynebacte
30		7.	7	7	CAE48694	Cae48694 corynebac
31		7.	~	7	Q7MWT7	Q7mwt7 porphyromon

	Q9eb09 sesbania mo	Q7qnq2 giardia lam	Q92110 rhizobium m	Q8tw68 methanopyru	Q854q1 mycobacteri	Q9vuy2 drosophila	Q8cjz5 streptomyce	Q6yznl oryza sativ	Bad03478 oryza sat	Bad03752 oryza sat	Q82r39 streptomyce	Q9m5k9 euphorbia e	Q84sv9 oryza sativ
Q9L374	Q9EB09.	Q7QNQ2	Q92L10	OSTW68	085401	Q9VUY2	Q8CJZ5	O6YZN1	BAD03478	BAD03752	Q82R39	Q9M5K9	Q84SV9
8	~	~	~	7	7	7	0	7	7	7	(1	~	73
94	160	291	297	311	409	451	482	546	546	546	645	219	479
37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.0	37.0
43	43	43	43	43	43	43	43	43	43	43	4.3	42.5	42.5
32	33	34	35	36	37	38	39	40	41	24	43	44	45

ALIGNMENTS

RESULT 1 BUB1_SCHPO ACC BUB1_SCHPO BUB1_SCHPO BUB1_SCHPO BUB1_SCHPO BUB1_SCHIZO BUB1_SCHIZ	SCHEPO STANDARD; PRT; 1044 AA. BUJI SCHEPO STANDARD; PRT; 1044 AA. D4751; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 44, Last amotation update) Checkpoint serine/threonine-protein kinase bubl (EC 2.7.1.37). Checkpoint serine/threonine-protein kinase bubl (EC 2.7.1.37). Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomyces. Schizosaccharomyces.	[1] SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION. STRAIN=SP011; MEDLINE=99085059; PubMed=9864354; Bernard P., Hardwick K.G., Javezrat JP.; Bernard P., Hardwick K.G., Javezrat JP.; Fission yeast Bubl is a mitotic centromere protein essential for the spindle checkpoint and the preservation of correct ploidy through mitosis."; mitosis."; Gell Biol. 143:1775-1787(1998).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=972, MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724; MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724; MEDLINE S., Basker S., Basker S., Baskam D., Bowman S., Sqouros J., Peach N., Hayles J., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Holroyd S., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moole S., Mungall K., Murphy L., Niblett D., Odell C.,	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B., Ruther S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares B., Squares S., Stevens K., Taylor K.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Welljens I., Vanstrels B. Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambitt R., Purnell B., Goffeau A., Cadieu B., Dreanc S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; Mature 415:871-880(2002).
	SCHPO BUBL SCHPO BUBL SCHPO BUBL SCHPO BUBL SCHPO 16-OCT-2001 (Rel. 40 16-OCT-2004 (Rel. 40 16-OCT-2004 (Rel. 44 Checkpoint serine/th Name=bubl; ORFNames= Schizosaccharomyces Bukaryota; Fungi; As Schizosaccharomyces Schizosaccharomyces Schizosaccharomyces Schizosaccharomyces NCBI_TAXID=4896;	[1] SEQUENCE FROM N SEQUENCE FROM N MEDLINE=9908505 Bernard P., Haz "Fission yeast spindle checkpto mitosis." U. Cell Biol. 1	UENCE AINES LINES d V., duros oks P 11ins tles royd royd	Rutherford K., Skelton J., Skelton J., Skelton J., Skelton J., Skelton J., Skelton J., Wedbelden J., Wedbelden J., Wedbelden J., Wedbelden K., Lank Borzym K., Lank Borzym K., Lank Goffeau A., Caudoffean R.R., Caudons R.R., Crulbominguez A., Icerutti L., Loi Shpakovski G.V Shp

SO THE PERSON DESCRIPTION OF THE PERSON DESC

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PRAVPFPVRCACEFLMQAF 143
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    ZF_FYVE; 1.
; 66440 MW;
                                                           Similarity 63.6%; 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.1%;
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nes 8; Conservative
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                   2 RGAPMWLRCVC 12
                                                                                                                               36 RSRPMWLACTC 46
                                                                                                                                                                                                                                                                  Phytochrome (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
                 579 AA;
                                         Query Match
Best Local Similarity
     PS50178;
                                                                                                                                                                                                                              01-MAR-2001
                                                                                                                                                                                                                                          01-MAR-2001
                                                                                                                                                                                                                                                    01-JUN-2003
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ID DHAQ ACEPO
AC P17201;
                                                                                                                                                                                                                                                                                  Name=phyP;
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SEQÜENCE
    PROSITE;
                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                              09FSA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                 Q9FSA3
                                                                        Matches
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                                                                                                                                                                       RESULT 3
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ID Q9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Ruropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                       Gaps
                                                    -!- PTM: Autophosphorylated (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. BUB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mcuse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
          phosphorylation of bub3.
CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CSTBL/63.

A Brathwaite M., Waeltz P., Schlessinger D., Nagaraja R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

R BMBL; AY301264; AAP45200.1; -.

GO; GO:0008270; F:zinc ion binding; IEA.

R InterPro; IPR001849; PH.

R InterPro; IPR001219; RhGEF.

R InterPro; IPR000306; Znf_FYVE.

R Pfam; PF001621; RhGEF.

R Pfam; PF001621; RhGEF.

R SMART; SM00064; FYVE; 1.

R SMART; SM000233; PH; 2.

R SMART; SM000233; PH; 2.

R SMART; RN000233; PH; 2.

R SMART; RN00023; PH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
stabilize the spindle during mitosis. Catalyzes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Fgd2-like protein splice form II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             579 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.5%; Score 50; DB
53.3%; Pred. No. 49;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                     SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                    EMBL; AF064796; AAC98348.1; -. EMBL; AL035259; CAA22865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 MWLRCVCOMLETKFL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 VWYRCIEWLLETRFL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                               PIR; T43800; T43800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7TSE3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
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QQ à

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Schoeled The EMBL/GenBank/DDBJ databases.

Schoeled (JAN-2000) to the EMBL/GenBank/DDBJ databases.

B. Schmidted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

B. Schmidted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

R. Schoeled (JAN-2000) to the EMBL/GenBank/DDBJ databases.

B. RO'S GO:00006351; P:red, far.red light photoreceptor activity; IEA.

B. GO:00006355; P:red, far.red light photorensduction; IEA.

GO:00006355; P:red, far.red light photorensduction; IEA.

B. GO:00006355; P:redlation of transcription, DNA-dependent; IEA.

B. GO:00006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro: IPR001294; Phytochrome.

B. Ffam: PF019050; GAF.

P. Ffam: PF019050; Phytochrome.

P. Ffam: PF019050; Phytochrome.

B. RINTS; PR01033; PHYTOCHROME.

B. SNART; SM00065; GAF: I.
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stangēria eriopus (Natal grass cycad).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Cycadophyta; Cycadales; Stangeriaceae; Stangeria.
NCBI_TaxID=34343;
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01-AUG-1990 (Rel. 15, Last sequence update)
05-AUG-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Membrane-bound aldehyde dehydrogenase [pyrroloquinoline-quinone]
precursor (EC 1.2.99.3) (ALDH).
Acetobacter polyoxogenes.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraces; Acetobacter.
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                                                             41.7%; Score 48; DB 2; Length 579; 63.6%; Pred. No. 58; 1. Indels iive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 2; Length 188;
Pred. No. 29;
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C2CEF594A797F4EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 16, Created) (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    188 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00245; PHYTOCHROME 1; 1. PROSITE; PS50046; PHYTOCHROME 2; 1.
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Gaps

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307 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 PRGGTVWLGSLIQLLE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PRGAPMWLRCVCQMLE 16
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36 PRGGTVWLGSLIQLLE
                                                                                                                                                     2 RGAPMWLRCVCQML 15
                                                                                                                                                                                                                                  26 RGAPLWLRARFOAL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.00
The second 
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                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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ses 8; Conserv
                        Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=paaX2;
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                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                     "Nucleotide sequence of the membrane-bound aldehyde dehydrogenase gene
                                                                                                                                                                                                                                      -i- CATALYTIC ACTIVITY: An aldehyde + acceptor + H(2)O = a carboxylate + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: PQO.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane-bound aldehyde dehydrogenase [pyrrologuinoline-quinone].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pearse R.V. Jr., Vogan K.J., Tabin C.J.;

"Ptcl and Ptc2 Transcripts Provide Distinct Readouts of Hedgehog Signaling Activity during Chick Embryogenesis.";

Dev. Biol. 0.0-0(2001).

EMBL, AF409055, AAX97655.1; -...

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0008188; F:hedgehog receptor activity; IEA.

InterPro; IPR004766; Patchedtm.recept.

InterPro; IPR004766; Patchedtm.recept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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TIGREAMS; TIGR01409; TAT Signal seq; 1.
Direct protein sequencing; Inner membrane; Oxidoreductase; PQ0;
Signal; Transmembrane.
                                                Tamaki T., Horinouchi S., Fukaya M., Okumura H., Kawamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 913;
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Last annotation update)
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Pred. No. 1.1e+02;
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InterPro; IPR008274; Aldxan_dh_bind.
InterPro; IPR006311; Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF02460, Patched, I.
TIGRFAMS, TIGRO0918, 2A060602, 1.
PROSITE, PS50156, SSD, 1.
                                                                                                                                                                 from Acetobacter polyoxogenes."; J. Biochem. 106:541-544(1989).
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a 40.9%;
Similarity 61.5%;
B; Conservative
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                                                                                                                                                                                                                                                                                                                                   STRAIN=Y2;
Bartolome-Martin D., Martinez-Garcia E., Mascaraque V., Rubio J.,
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                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
NCBI_TaxID=198931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perera J., Alonso S.; "Characterization of a second functional gene cluster for catabolism of phenylacetic acid in Pseudomonas sp. strain Submitteid (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AJS79894; CAE45100.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                        Perera J., Alonso S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
EMBL, AJ579894, CAE45100.1;
InterPro; IPR009058; Wing hlx DNA bnd.
SEQUENCE 307 AA, 34884 WW; 72348C9C6E3CA676 CRC64;
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SEQUENCE 307 AA; 34884 MW; 72348C9C6E3CA676 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transcriptional repressor.
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39.1%;
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                                                                                                                                     8; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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Q82J76
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIR-BES11, and DSM 6160;
MEDI.NE=97385083; PubMed=9238099;
Thurner C.A., Vela C., Thony-Meyer L., Meile L., Teuber M.;
Thurner C.A., orla Gonetic characterization of the acetaldehyde de hydrogenase complex from Acebacter europaens;";
Arch. Microbiol. 168:81-91(1997).
                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales,
Acetobacteraceae, Gluconacetobacter.
NCBI_TaxID=33995;
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STRAIN=YS-314;
MEDIINB=Z2722372; PubMed=12840036;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 2; Length 773;
Pred. No. 1.6e+02;
2; Mismatches 4; Indels
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: 3B549B655BE63F56 CRC64;
                                                                                                                                                            Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                     773 AA.
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TIGRFAMs; TIGR01409; TAT_Signal_seq; 1.
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                                                                                                                               Created)
                                                                     PRT;
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                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Last Aldehyde dehydrogenase precursor.
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EMBL; AP005220; BAC18752.1; -.
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53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-DES11, and DSM 6160;
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OrderedLocusNames=CE1942;
Corynebacterium efficiens.
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Best Local Similarity 53.8
Matches 7; Conservative
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                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                 Acetobacter europaeus.
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01-JAN-1998
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Q8FP46
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EMBL; AB070940; BAB69186.1; -
GO: GO:0009366; C:enterobactin synthetase complex; IEA.
GO: GO:0000287; F:holo-(acyl-carrier protein] synthase activity; IEA.
GO: GO:0000287; F:nagnesium ion binding; IEA.
GO: GO:0000239; P:enterobactin biosynthesis; IEA.
GO: GO:0009239; P:enterobactin biosynthesis; IEA.
InterPro; IPR008278; 4-PPT_transf.
InterPro; IPR008278; 4-PPT_transf.
InterPro; IPR008278; Enbac_synthetD.
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MEDLINE=21477403; PubMed=11572948;

Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
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                                                                                                 2; Length 120;
                                                                                                                                                              Indels
Complete proteome; Hypothetical protein.
SEQUENCE 120 AA; 13296 MW; 9C8D11681057EAD0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative phosphopantetheinyl transferase.
Name-pptAl; OrderedLocusNames=SAV2905;
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                                                                                              Score 45; DB
Pred. No. 39;
                                                                                                                                                        3; Mismatches
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PRINTS; PR01399; ENTSNTHTASED.
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PRT;
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InterPro; IPR000198; RhoGAP.
InterPro; IPR008936; Rho_GAP.
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26,
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PROSITE; PS50238; RHOGAP; 1.
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01-MAR-2004 (TrEMBLrel.
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Name=NCU04534.1;
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SECUENCE FROM N.A.
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 12 days embryo female mullerian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6820430Nl0 product:similar to MACGAP (Fragment).
                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003).

EMBL, AP005033; BAC70661;

GO; GO:00009366; C:enterobactin synthetase complex; IEA.

GO; GO:0000887; F:holo-[acyl-carrier protein] synthase activity; IEA.

GO; GO:0000887; F:masferase activity; IEA.

GO; GO:00009239; P:enterobactin biosynthesis; IEA.

GO; GO:00006731; P:enterobactin biosynthesis; IEA.
                                                                                                                                                                                                                                                                              Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
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STRAIN=C57BL/6J; TISSUE=Mullerian duct includes surrounding region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CS7BL/60; TISSUE=Mullerian duct includes surrounding region;
MEDLINE=21085660; Pubmed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                  MEDLINE=21477403; PubMed=11572948; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 260;
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                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Interpro, IPR003542; Enbac_synthetD.
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                                                                                                                                                                                                                                          STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome, Transferase.
SEQUENCE 260 AA; 28003 MW;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
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Matches
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/G0; TISSUE=Mullerian duct includes surrounding region;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
The FANTOM Consortium, the RINTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; whallysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAINS—CSTBL/6J; TISSUE=Mullerian duct includes surrounding region; MEDLINE=20530913; PubMed=11076861; Shibate R., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Hazama M., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik Nithegarated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 371;
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Last sequence update)
Last annotation update)
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131 PRSAPLWLR 139
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                                                     RESULT 15
                                                                      Q8K0Q5
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                                                                      RAGINGARY AND S.E., Borkovich K.A., Selker E.U., Read N.D., RAGINER Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., R. Otti D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schulte U., RA Goti D., Ianakiev P., Pedersen D., Malson M., Mashburne M., Schulte U., RA Kothe G.U., Janakiev P., Ramus W., Staben C., Marcotte E., Greenberg D., RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., RA Roy A., Foley K., Naylor J., Itomann N., Barrett R., Osmani S.A., RASTSTOONS S., Rasmussen C., Metzenberg R.L., Pertir B.J., Kroken S., RA Gogoni C., Macino G., Carcheside D., Li W., Pratt R.J., Osmani S.A., RAGONI C., Macino G., Carcheside D., Li W., Pratt R.J., Osmani S.A., RAGONI C., Macino G., Carcheside D., Li W., Pratt R.J., Osmani S.A., Raden C., Plack L., Mannaupt G., Ebbole D.J., Freitag M., Ardengo C., Alex L., Mannaupt G., Ebbole D.J., Freitag M., Natvig D.O., Alex L., Mannaupt G., Ebbole D.J., Freitag M., Natvig D.O., Alex L., Mannaupt G., Ebbole D.J., Freitag M., Natvig D.O., Alex L., Mannaut E.S., Nusbaum C., Birren B., Natvig C.C. (2003).

C. -- SIMMARITY: Contains 7 WD repeats.

C. -- SIMMARITY: Contains 7 WD repeats.

C. -- SIMMARITY: Mathematic Shown here is derived from an EmBL, Genbank, DBU whole genome shotgun (WGS) entry which is Brell; AABKO1060; WD40.

B. FRENTE; PRO00509; Lish.

B. RROSITE; PRO00509; Lish.

B. RROSITE; PRO00678; WD40.

B. RROSITE; PRO00678; WD40.

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Emericella nidulans (Aspergillus nidulans).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 2; Length 441;
Pred. No. 1.3e+02;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.1%; Score 45; DB 2; Length 486; 77.8%; Pred. No. 1.5e+02; ive 1; Mismatches 1; Indels
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBL_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sold-Raggi G., Aguirre J.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY254382; AAP13095.1; -
SEQUENCE 486 AA; 54446 MW; C5C902584D8F2AIF CRC64;
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Last annotation update)
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last amog
01-UUN-2003 (TrEMBLrel. 24, Last amog
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42.1%;
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Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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1 PRGAPMWLR 9

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SEQUENCE FROM N.A.

STATIN-EVB/N; TISSUBE-Liver;

RA MEDLINE=2388257; Pubmed=12477932;

RA MEDLINE=2388257; Pubmed=12477932;

RA Alteschul S.F., Zeeberg B.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B.A., Buecow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RACHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Bosak S.A., Mochan D.W., Sodergren E.J., Lu X., Gibbs R.A.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Halton B., Madan A., Young A. C., Garchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A. C., Shevchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A. C., Shevchenko Y., Bouffard G.G.,

R. Rozywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human and mall analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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52.9%; Pred. No. 1.9e+02;
tive 3; Mismatches 5; Indels
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SMART; SM00224; RhoGAP; 1.
PROSTIE; PS50238; RHOGAP; 1.
SEQUENCE 663 AA; 74930 MW; BB9ED06B8S0FEF41 CRC64;
                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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368 GAAMRIKNLCQELEAKF 384
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                                                   01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
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PRELIMINARY;
                                                                                                                                                                                                               Mus musculus (Mouse).
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                                                                                                                                                                                  Name=Arhqap18;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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; Search time 85.5 Seconds
(without alignments)
83.913 Million cell updates/sec October 26, 2004, 06:09:56; Run on:

US-10-066-965A-4 Title: Perfect score:

115 1 PRGAPMWLRCVCQMLETKFL 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 Total number of hits satisfying chosen parameters:

2002273 seqs, 358729299 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:*
geneseqp2001s:*
geneseqp2003s:*
geneseqp2003bs:*
geneseqp2004s:* A_Geneseq_23Sep04:* 1: genesernleser geneseqp1980s:* geneseqp1990s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description		1 Aao09931 Human pol		Aap91653 Membra	S Aau31146 Novel hum	Adc87493			Ade95594	Abg25840	Aam21627	Abb43988	Aam38254	Aam37929	Abb26897	3 Abb27163 Protein	3 Aam77713 Human bon	0 Aam64990 Human bra	7 Abg59367 Human liv		Abg46741 Human	Aau30945 Novel	2 Adf74142 Human nov	4 Abo75594 Pseudomon		
SUMM		ΩI	1 1 1 1 1 1	AA009931	AA009705	AAP91653	AAU31146	ADC87493	ABG01589	ADE95598	ADE95594	ABG25840	AAM21627	ABB43988	AAM38254	AAM37929	ABB26897	ABB27163	AAM77713	AAM64990	ABG59367	ABG47050	ABG46741	AAU30945	ADF74142	AB075594	AA010516	
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75	ADF78159	AAE31060	AA015858	AAU72900	AAU05396	ADQ17316	ABG74786	ABG22489	ABG30084	ABO54483	AAU60604	ABM57123	ADM26562	AAU20410	ABB67753	AAB09041	AAU40132	ABM36651	ABU49786
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133	194	243	413	1094	26926	26926	31267	884	884	57	62	62	311	441	451	1422	261	261	622
38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	37.8	37.8	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.0	37.0	37.0
44	44	44	44	44	44	44	44	43.5	43.5	43	43	43	43	43	43	43	42.5	42.5	42.5
26	27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
               AA009931 standard; protein; 112 AA.
                                                                  Human polypeptide SEQ ID NO 23823.
                                                                                                                                                                                                                                           rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                 28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                 26-FEB-2001; 2001WO-US004927
                                                 (first entry)
                                                                                                                                                                                                                                                           WPI; 2001-514838/56.
N-PSDB; AAI89862.
                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                               WO200164835-A2
                                                                                                                                Homo sapiens.
                                                 06-NOV-2001
                                                                                                                                                                07-SEP-2001.
                                 AAO09931;
RESULT 1
         AA00993
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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.

Claim 20; SEQ ID NO 23823; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI79941-AAI99841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and

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1 PRGAPMWLRCVCQML 15
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                                                                                                                                                                  AAP91653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene
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                                                                                                              AAP91653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU31146
                                                                                              RESULT
                                                                                                                                 원
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                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to ovtokine, call proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemacopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 23597; 1399pp + Sequence Listing; English.
                                                                                                           Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 78;
                                                                                                                                               4; Indels
                                                                                                              4;
                                                                                                           43.5%; Score 50; DB 4 56.2%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 4
Pred. No. 6.3;
2; Mismatches
                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 23597.
                                                                                                                                                                                                                                                                                                     AA009705 standard; protein; 78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.6%;
                                                                                                                                                                                 1 PRGAPMWLRCVCQMLE 16
                                                                                                                                                                                                         PRGAAAYVRCVSALLE
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                              9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                         Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-514838/
N-PSDB; AAI89636.
                                                                       Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-2001
                                                                                                                                                                                                                                                                                                                                        AAC09705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT,
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                    AAC09705
ID AACC
                                                                                                                                                                                                                                                                  RESULT 2
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SO X C C C C C C C C C C C C X S X L L X X B X B X X B

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quinoline as prosthetic gp. It is used in oxidn. of ethanol to acetic acid, and in oxidative decomposition of aldehydes that give food a bad taste. The new plasmids claimed increase this enzyme content in cells. A altoacetigenes strain MH-24 FERM BP-491 is the source DNA. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR 2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e for membrane-bound aldehyde dehydrogenase - derived from Acetobacter used to transform acetic acid bacteria to enhance prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawamura Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxidises aldehyde to corresp. acid with the aid of pyrrolo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                     Acetobacter; aldehyde dehydrogenase; acetic acid fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 1; Length 773;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; vaccination; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okumura H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Izumo H,
                                                                                                                                                                                                                                                                                                       Membrane-bound aldehyde dehydrogenase.
                                                                                                                 AAP91653 standard; protein; 773 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted protein #1637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tamaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU31146 standard; protein; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Fig 3; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAKA-) NAKANO VINEGAR CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89EP-00103936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89JP-00033775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.9%;
61.5%;
22
                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RGAPMWLRCVCQM 14
PRGAPACLRCLSALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tayama K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-265358/37.
                                                                                                                                                                                                                                                                                                                                                                                                   Acetobacter aceti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN90816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 773 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-1989;
                                                                                                                                                                                                                                                            22-JAN-1990
                                                                                                                                                                                                           27-AUG-2003
25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                               EP332120-A.
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Gaps

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Indels

4;

9; Conservative

Matches

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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
                                                                                                                                                                                                                                                                      New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.0%; Score 46; DB 7; Length 274; 53.3%; Pred. No. 63; cive 2; Mismatches 5; Indels
                                                                                         (NDAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                          Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 1946; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #1580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG01589 standard; protein; 634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
18-JUN-2002; 2002EP-00013517.
                                            18-JUN-2001; 2001JP-00246789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PRGAPMWLRCVCQML 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73
                                                                                                                                                                                                         WPI; 2003-315783/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS65776.
                                                                                                                                                                                                                              N-PSDB; ADC87492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001.
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                                                                                                                                                             Suwa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
       stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%; Score 46; DB 4; Length 88; 50.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 410; 765pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human GPCR protein SEQ ID NO:1946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PRGAPMWLRCVCQMLETKFL 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC87493 standard; protein; 274
                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT;
                                                                                                                                                                                                           16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                        18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.v.
Best Local 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-611725/70
                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 88 AA;
                                                                                                                     WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy
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                                                                                                                                                               25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                      Tang YT,
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RESULT 5 ADC87493

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Gaps

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ADE95594;
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ADE95594
   à
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                          The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) is useful in gene therapy techniques to restore normal cuspill for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food cuspill for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food consupplement. (II) and (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in expressing to of sites expressing (II). (I) and (II) are useful or treating disorders involving aberrant protein expression or biological activity. The diagnostics, forensics, gene mapping, identification of mutations in chaptering and to produce other types of data and products dependent on DNA and and and to produce other types of data and products dependent on DNA and and an orial sequences. ABG00010-ABG00377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the control of control of the control of the control of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; biochemical stimulation; physiological stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 4; Length 634;
Pred. No. 1.4e+02;
1; Mismatches 3; Indels
Claim 20; SEQ ID NO 31948; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE95598 standard; protein; 195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0341477P.
2001US-0341540P.
2001US-0342592P.
2001US-0344297P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.0%;
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2001US-0341346P.
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Best Local Similarity 63.00
Pertage 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NOVX22c protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 634 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003050245-A2.
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17-DEC-2001;
20-DEC-2001;
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ADE95598
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This invention relates to novel NOVX proteins, and the DNA sequence which encode them, having properties related to stimulation of biochemical or physiological responses in a cell, a tissue, an organ or an organism. Compounds which modulate the proteins of the invention may have cardiant, antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic, antiarthritic, antidiabetic, nephrotropic, dermatological, immunosuppressive, anti-HIV, antiinflammatory, neuroprotective noorropic, antipsoriatic, antianthaniatic neuroleptic, antidepressant, antiallergic or synaecological activities. The DNA sequences of the invention may be useful for gene therapy whilst the protein sequences may allow the development of a vaccine. The protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The invention may be useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The invention may be useful in diagnosing, treating or preventing NOWX-associated disorders, for example cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin disorders, inflammation, multiple solerosis, Alzheimer's disease, Parkinson's disease, asthma, schizophrenia, depression, allergies or hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is the amino acid sequence of the human NOWX22c protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chillakuru RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA, Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X; Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphey R; Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG; Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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Pred. No. 55;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 130; 211pp; English.
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15-MAY-2002; 2002US-03809B1P.
17-MAY-2002; 2002US-0381495P.
28-MAY-2002; 2002US-0383534P.
29-MAY-2002; 2002US-0383744F.
29-MAY-2002; 2002US-0383744P.
29-MAY-2002; 2002US-0384024P.
07-MUG-2002; 2002US-0401788P.
26-MUG-2002; 2002US-0401788P.
31-0CT-2002; 2002US-0401788P.
02-DEC-2002; 2002US-07406353P.
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66.7%;
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Best Local Similarity 66.7,,
Best Local Similarity 57.7,
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                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
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N-PSDB; ADE95597.
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cardiati, antiarteriosclerotic; hypotensive, cytostatic; anorectic; antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological; immunosuppressive, anti-HIV, antidiabatory; neuroprotective; nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroprotective; antidepressant; antiallergic; gynaecological; gene therapy; vaccine; NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis; psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis; Alzheimer's disease; Parkinson's disease; asthma; schizophrenia; depression; allergy; fertility disorder; NOVX22a. /note= "OTHER= May be substituted by Tyr as a result single nucleotide polymorphism" 'note= "OTHER= May be substituted by Pro as a result protein; biochemical stimulation; physiological stimulation; single nucleotide polymorphism" 220 Location/Qualifiers 55 /label= OTHER /label= OTHER Misc-difference Misc-difference Homo sapiens NOVX

WO2003050245-A2

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19-JUN-2003

03-DEC-2002; 2002WO-US038594

2001US-0336600P. 2001US-0338285P. 2001US-0341346P. 17-DEC-2001; 17-DEC-2001; 20-DEC-2001; 05-DEC-2001; 07-DEC-2001;

2001US-0341477P 2001US-0341540P 2001US-0342592P 2001US-0344903P 2002US-0319288P 2002US-0380981P 2002US-0380981P 2002US-0380981P 15-MAY-2002; 2 17-MAY-2002; 2 28-MAY-2002; 3 31-DEC-2001; 17-APR-2002; 28-MAY-2002;

2002US-0383744P. 2002US-0383829P. 2002US-0384024P. 2002US-0401788P. 2002US-0406353P. 31-OCT-2002; 2002US-00401788 02-DEC-2002; 2002US-00406353 29-MAY-2002; 29-MAY-2002; 07-AUG-2002; 26-AUG-2002;

(CURA-) CURAGEN CORP.

Chillakuru RA; Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru J Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X; Jefffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphey R; Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG; Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong I

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WPI; 2003-513974/48. N-PSDB; ADE95593.

or New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing pharmacogenomics

Claim 2; SEQ ID NO 126; 211pp; English.

This invention relates to novel NOVX proteins, and the DNA sequence which encode them, having properties related to stimulation of biochemical or physiological responses in a cell, a tissue, an organ or an organism. Compounds which modulate the proteins of the invention may have cardiant,

ï antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic, antiarthritic, antidiabetic, nephrotropic, dermatological, immunosuppressive, anti-HTV, antiinflammatory, neuroprotective, noctropic, antiparkinsonian, antiasthmatic, neuroleptic, antidepressant, antiallergic or gynaecological activities. The DNA sequences of the invention may be useful for gene therapy whilst the protein sequences may allow the development of a vaccine. The protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The invention may be useful in diagnosing, treating or preventing NOVX associated disorders, for example The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cardiomyopathy, atheroscierosis, hypertension, cancer, obesity, rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease, Parkinson's disease, asthma, schizophrenia, depression, allergies or fertility disorders. The nucleic acids may further be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is the amino acid Gaps New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder. 1, Length 264; Indels sequence of the human NOVX22a protein of the invention 2; Score 45.5; DB 7; Pred. No. 73; 1; Mismatches 2; Claim 20; SEQ ID NO 56199; 103pp; English. Novel human diagnostic protein #25831. ABG25840 standard; protein; 482 AA. 39.68; 66.78; 30-MAR-2001; 2001WO-US008631. Tang YT; 31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167 (first entry) 253 PLGAPOWV-CVC 263 8; Conservative 1 PRGAPMWLRCVC 12 Drmanac RT, Liu C, WPI; 2001-639362/73 Query Match Best Local Similarity Matches 8; Conserv (HYSE-) HYSEQ INC. N-PSDB; AAS90027. Sequence 264 AA; WO200175067-A2. biodiversity. Homo sapiens 11-OCT-2001. 18-FEB-2002 ABG25840; RESULT 9 ABG25840 d ò

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genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPS are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical
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expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #8061 encoded by probe for measuring cervical gene expression.
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Pred. No. 1.3e+02;
3; Mismatches 3;
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244 PRTHPVWVRTRGRRCTCQL 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                  Sequence 482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer
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epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                           Peptide #11494 encoded by human foetal liver single exon probe.
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                                                                                                                         Score 45; DB 4; Length 32;
Pred. No. 12;
1; Mismatches 0; Indels
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Pred. No. 12;
1; Mismatches
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                                                                                                                                                                                                                                                                                                  ABB43988 standard; peptide; 32 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000; 2000US-0207456F.
30-UTN-2000; 2000US-0608498.
30-AUG-2000; 2000US-0032866.
21-SEP-2000; 2000US-0234687P.
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                                                                                                                         39.1%;
Similarity 85.7%;
6; Conservative
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                                                                                                                                    Local Similarity
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Best Local Similarity
                                                                                             Sequence 32 AA;
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Matches
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04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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                                                      WO200157272-A2.
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                  Homo sapiens
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                                                                                                                                                                                                               Peptide #12291 encoded by probe for measuring placental gene expression.
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                                                                                             AAM38254 standard; protein; 32 AA.
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2000US-00608408.
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27-SEP-2000; 2000US-0236359P.
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Best Local Similarity 85.7%;
Matches 6; Conservative
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26 MWMRCVC 32
                                                                                                                                                                                                                                                                            genetic disorder
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30-JUN-2000;
03-AUG-2000;
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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 38198; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
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                                                                                        26-MXY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234539P.
04-OCT-2000; 2000GB-00024263.
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30-JAN-2001; 2001WO-US000663
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0;
                                                                                                                                                              The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA2155-ABA4136). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, stading, stading, nonitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. Wipo.int/pub/published_pct_sequences
                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                         Claim 15; SEQ ID NO 28667; 530pp; English.
                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB27163 standard; protein; 32 AA.
                                  (MOLE-) MOLECULAR DYNAMICS INC.
 27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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85.7%;
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                                                          Hanzel DK,
                                                                                WPI; 2001-488899/53
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                            Sequence 32 AA;
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                                                          Penn SG,
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Protein #9162 encoded by probe for measuring heart cell gene expression.

Human, gene expression, heart, microarray, vascular system, cardiovascular disease, hypertension, cardiac arrhythmia,

congenital heart disease.

WO200157274-A2 Homo sapiens

09-AUG-2001.

Rank DR;

Chen W,

Hanzel DK,

Penn SG, (MOLE-)

WPI; 2001-488899/53

MOLECULAR DYNAMICS INC

26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

2000US-0236359P. 2000GB-00024263.

27-SEP-2000;

30-JAN-2001; 2001WO-US000666

2000US-0180312P

04-FEB-2000;

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0;
                                                                                                      The present invention relates to single exon nucleic acid probes for ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                 Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                     Claim 15; SEQ ID NO 28933; 530pp; English.
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ne : 86.5 secs
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October 26, 2004, 06:45:25; Search time 64.25 Seconds (without alignments) 100.781 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO5_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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| cgn2 6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1364641 seqs, 323758627 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                            115
1 PRGAPMWLRCVCQMLETKFL 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                         Title:
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					SUMMARIES		
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esult No.	Score	Query Match	Query Match Length DB ID	DB	ID	Description	
	115	100.0	20	14	4 US-10-066-965A-4	Sequence 4, Appli	
2	115	100.0	20	14	US-10-066-965A-23	Sequence 23, Appl	
(4)	96	83.5	20	14	US-10-066-965A-3	Sequence 3, Appli	
4	96	83.5	20		US-10-066-965A-22	Sequence 22, Appl	
יעי	200	43.5		٠.	US-10-369-493-22713	Sequence 22713, A	
ب ر	49	42.6		٠.	US-10-437-963-142466	Sequence 142466,	
7	46	40.0	274		US-10-017-161-2300	Sequence 2300, Ap	
- α	46	40.0		•	US-10-292-798-1946	Sequence 1946, Ap	
0	45.5	39.6		15	US-10-309-290-130	Sequence 130, App	
0	45.5	39.6		15	US-10-309-290-126	Sequence 126, App	
1 7	45	39.1		σ	US-09-864-761-42195	Sequence 42195, A	
12	45	39.1		σ	US-09-864-761-42461	Seguence 42461, A	
13	45	39.1		14		Sequence 10442, A	

133679		ω	Sequence 627, App			Sequence	Sequence 2, Appli	Sequence 42489, A		Sequence 28117, A	Sequence 125793,	Sequence 125130,	Sequence 235647,	Sequence 123986,	Sequence 121604,	Segue	Sequence 86, Appl	Sequence 267231,	edne	edne	Sequence 166717,	Sequence 191710,	Sequence 197107,	Sequence 77710, A	Sequence 183, App	Sequence 236745,	ěďa	21198	Sequence 144556,	651		
-133	.369-493-	01 - 554	325-297-6	US-10-081-051-2	US-10-106-534-6	US-10-27	US-09-759-508B-2	US-10-425-114-4248	US-10-424-599-2	US-10-029-386-2	US-10-437-96	US-10-437-963-1	US-10-424-599-2	US-10-437-963-1	US-10-437-963-1	US-10-156-761-7854	-424-550B-8	US-10-4	US-10	US-10-4	US-10-4	US-10-4	US-10-43	US-10-282-122	US-10	US-10-424-599	US-10-424-599	US-10-424-599	US-10-424-599	US-10-106-698		100 111 01-20
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39.1	39.1	38.3	38,3	38.3	38.3	38.3	38.3	37.8	37.8	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.0	37.0	37.0	37.0	37.0	37.0	37.0	36.5	36.5	36.5	36.5	Ġ	36.5		ċ
45	4.5	4 4	44	4			44	m	43.5	43	43	43	43	43	43	4.3	43	42.5	42.5	42.5		42.5			~ ₹	. 4	42	42	42	4.2	3 5	7#
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ALIGNMENTS

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     Sequence A Application US/10066965A

Subjication No. US20030143626A1

Subjicant: Defent Rocer

APPLICANT: COHEN, BARAK A.

TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS

TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS

TITLE OF INVENTION: US/10/066, 965A

CURRENT FILING DATE: 2002-12-09

NOWHER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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US-10-066-965A-4
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100.0%; Score 115; DB 14;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 20; Conservative 0; Mismatches 0;
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US-10-066-965A-23
Sequence 23, Application US/10066965A
; Publication No. US20030143626A1
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                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
US-10-066-965A-4
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SOFTWARE: Patentin Ver.
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ADDITION: BRENT, ROGER

ADDITION: BRENT, ROGER

TILLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS

TILLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS

FILE REPERENCE: EGYP 3.0-015

CURRENT APPLICATION NUMBER: US/10/066,965A

NUMBER OF SEQ ID NOS: 33

SEQ ID NO 23

TYPE: TENNING DATE: 20

TYPE: TYPE: THE TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS

TYPE: TENNING DATE: 20
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APPLICANT: COLAS, PIERRE
APPLICANT: BRENAT, BARAK A.
TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
FILE REFERENCE: EGYP 3.0-015
CURRENT APPLICATION NUMBER: US/10/066,965A
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATERTIN Ver. 2.1
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US-10-066-965A-22

Sequence 22, Application US/10066965A

Publication No. US20030143626A1

GENERAL INFORMATION:

APPLICANT: COLAS, PIERRE

APPLICANT: COHEN, BARBAK A.

TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS

FILE REFERENCE: EGYP 3.0-015
                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-066-965A-23
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0
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100.0%; Score 115; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels
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85.0%; Pred. No. 3.8e-07;
iive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/10066965A; Publication No. US20030143626A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PRGAPMWLRCVCQMLETKFL 20
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ORGANISM: Artificial Sequence
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LENGTH: 20
TYPE: PT CRGANISM: Artificial Sequence
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Best Local Similarity 85.0
Matches 17; Conservative
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US-10-066-965A-3
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Sequence 142466. Application US/10437963
| Publication No. US20040123343A1
| CENDERAL INFORMATION:
| APPLICANT: Exoa, Thomas J. |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Boutharov, Andrey A. |
| APPLICANT: Boutharov, Andrey A. |
| APPLICANT: Boutharov, Andrey A. |
| APPLICANT: Brabazuk, Brad |
| APPLICANT: Brank Brade |
| APPLICANT: Brank Brade |
| APPLICANT: Brad |
| APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
FURENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 1044
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                                                                                                                                                     FEATURE:
// OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-066-965A-22
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83;
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Pred. No. 3.8e-07;
1; Mismatches 2; Indels
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Sequence 22713, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Schizosaccharomyces pombe US-10-369-493-22713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PRGAPMWLRCVCOMLETKFL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PRGAPMWMRWVCQMLETMFL 20
                                                                                                                                                                                                                                                                                                                                              83.5%;
                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 53.2.
Best Local 8; Conservative
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Best Local Similarity
Matches 17; Conserv
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SEQ ID NO 22
LENGTH: 20
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APPLICANT: ASMA, MAXIKO
APPLICANT: ASMA, KIYOSHI
APPLICANT: ASMI, KIYOSHI
APPLICANT: ASMI, KIYOSHI
APPLICANT: ASMI, KIYOSHI
APPLICANT: ABURATANI, HIROJUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
CURRENT APPLICANTON NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-66-18
PRIOR FILING DATE: 2001-66-18
NUMBER OF SEQ ID NOS: 2070
SOUTHARE: PATENTING OF SEQ ID NOS: 2070
SEQ ID NO 1946
LERGIH: 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 14; Length 274; Pred. No. 96; 5; Indels 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (25)...(25)
OTHER INFORMATION: Variable amino acid
FEATURE:
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LOCATION: (187)...(187)
OTHER INFORMATION: Variable amino acid
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NAME/KEX: MOD RES
LOCATION: (222) .. (222)
OTHER INFORMATION: Variable amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD RES
LOCATION: (51)..(51)
OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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Sequence 1946, Application US/10292798 Publication No. US20030235833A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 130, Application US/10309290 Publication No. US20040023241A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alsobrook II, John P. APPLICANT: Anderson, David W. APPLICANT: Boldog, Ferenc L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                          Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD RES
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LOCATION: (45)...(
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US-10-309-290-130
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                             Gaps
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                                                                                                                                             Query Match 42.6%; Score 49; DB 16; Length 103; Best Local Similarity 45.0%; Pred. No. 14; Matches 9; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SUMM, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, WAKIKO
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ARIYAMA, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT APPLICATION NUMBER: UP 2001/246789
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ 1D NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 2300
                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_4346C.1.pep
US-10-437-963-142466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MOD_RES
LOCATION: (222)
OTHER INFORMATION: Variable amino acid
FEATURE:
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (248)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD RES
LOCATION: (45)
OTHER INFORMATION: Variable amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2300, Application US/10017161 Publication No. US20030143668A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                             1 PRGAPMWLRCVCQMLETKFL 20
                                                                                                                                                                                                                                                                                      17 PRARPCWLSCSCAAALLAFL 36
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PCGLPLFSRCVCVFL 84
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Best Local Similarity 53.33
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
              TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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FEATURE:
NAME/KEY: MOD RES
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LOCATION: (51)
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Gaps

Guo, Xiaojia Jeffers, Michael E. Ji, Weizhen

APPLICANT: APPLICANT:

RESULT 8 US-10-292-798-1946

APPLICANT

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TITLE OF INVENTION: THERAPEUTIC POLYPBPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILLING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 42195, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
ITTLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT PAPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
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Pred. No. 1.1e+02;
1; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURKEMN FILLING DATE: 2002-12-02
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/336,600
PRIOR APPLICATION NUMBER: 60/336,285
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR PILING DATE: 2001-12-12
PRIOR PELING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR PELING DATE: 2001-12-17
PRIOR PELING DATE: 2001-12-37
PRIOR PILING DATE: 2001-12-37
PRIOR APPLICATION NUMBER: 60/342,597
PRIOR PILING DATE: 2001-12-37
PRIOR PELING DATE: 2001-12-37
PRIOR PELING DATE: 2001-12-37
PRIOR PELING DATE: 2001-12-31
PRIOR PELING DATE: 2001-12-31
PRIOR FILING DATE: 2001-12-31
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-17
                                                   Malyankar, Uriel M.
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Starling, Gary
Taupier, Raymond J.
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                                                                           ler, Charles E.
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Patturajan, Meera
Peyman, John A.
                                                                                                                                                                               Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
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Zhong, Mei
                                                                                                                                                                                                                                                                                                                                           Voss, Edward Z
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Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-126
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Best Local Similarity
Matches 8; Conserv
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 274
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CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT APPLICATION NUMBER: 0/336,600
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-07
PRIOR PILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/344,597
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-37
PRIOR PILING DATE: 2001-12-37
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR PILING DATE: 2001-12-37
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR PILING DATE: 2001-12-37
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR APPLICATION NUMBER: 60/349,903
PRIOR APPLICATION NUMBER: 60/379,288
PRIOR APPLICATION NUMBER: 60/344,903
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Publication No. US20040023241A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P.
APPLICANT: Anderson, David W.
APPLICANT: Burgess, Catherine E.
APPLICANT: Chillakuru, Rajeev A.
APPLICANT: Gelinger, Shlomit R.
APPLICANT: Gelinger, Shlomit R.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gerlach, Valerie L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 130
LENGTH: 195
                                                                                                                 Peyman, John A.
Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
Smithson, Glenda
Starling, Cary
Taupier, Raymond J.
Voss, Edward Z.
                Malyankar, Uriel M
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Jeffers, Michael E.
                                           Miller, Charles E.
                                                                                           Patturajan, Meera
Peyman, John A.
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Zhong, Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 PLGAPOWV-CVC 194
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                                                                   Ryan
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; ORGANISM: Homo sapiens
US-10-309-290-130
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Best Local Similarity
                                                                   Murphey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-309-290-126
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Gaps
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CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.
CTHER INFORMATION: EXPRESSED IN PLACENIA, SIGNAL = 6.3
CTHER INFORMATION: EST_HUMAN HIT: C03546.1, EVALUE 3.00e-13
US-09-864-761-42461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 9; Length 32;
Pred. No. 19;
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ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Annomax Sequence Listing Engine vers. 1.1
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                           THILE OF LINGWILDS.

THILE OF LINGWILDS.

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELICATION NUMBER: US 60/180,312

PRIOR PELLING DATE: 2000-05-26

PRIOR PELLING DATE: 2000-06-26

PRIOR PELLING DATE: 2000-08-23

PRIOR PELLING DATE: 2000-08-23

PRIOR PELLING DATE: 2000-08-27

PRIOR PELLING DATE: 2000-09-27

PRIOR PELLING DATE: 2000-09-27

PRIOR PELLING DATE: 2000-09-27

PRIOR PELLING DATE: 2000-09-27

PRIOR PELLING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.1%;
85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 MWMRCVC 32
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Sequence 42461, Application US/09864761
Batent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3

OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8

US-09-864-761-42195
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19;
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           PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-06-30
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Pred. No. 19;
1; Mismatches
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OTHER INFORMATION: MAP TO AC021876.2
OTHER INFORMATION: EXPRESSED IN PLACE
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 469
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: W. Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbaruk, Brad
APPLICANT: Barbaruk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 133679
LENGTH: 294
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US-10-369-499-3310

Sequence 31310, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Greeory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
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Pred. No. 1.3e+02;
0; Mismatches 4; Indels
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39.1%; Score 45; DB 16; Length 294;
Best Local Similarity 47.4%; Pred. No. 1.4e+02;
Matches 9; Conservative 2; Mismatches 8; Indels
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US-10-437-963-133679
                 APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 133679, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10442
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Similarity 66.7%;
8; Conservative
SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PRGAPMWLRCVC 12
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 8; Conserv
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APPLICANT:
APPLICANT:
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TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
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US-09-252-991A-24340
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Sequence 38667, A
Sequence 53884, A
Sequence 7736, Ap
Sequence 39796, A
Sequence 23113, A
Sequence 23113, A
Sequence 1251, A
Sequence 3608, A
Sequence 3608, A
Sequence 3608, A
Sequence 3608, A
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                                                              ; Search time 22 Seconds (without alignments) 60.289 Million cell updates/sec
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Sequence 2,
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   /cgn2 6/ptodata1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata1/iaa/FB_COMB.pep:*
6: /cgn2 6/ptodata1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata1/iaa/PCTUS_COMB.pep:*
5.1.6
Compugen Ltd.
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US-08-444-86
US-09-124-5508-86
US-09-124-5508-86
US-09-270-767-38667
US-09-270-767-3884
US-09-252-991A-22897
US-09-621-976-7736
US-09-270-767-39796
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US-09-252-991A-23113
US-09-489-039A-12151
US-09-270-767-36276
US-09-270-767-51493
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US-09-270-767-43959
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US-08-469-260A-86
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                          - protein search, using sw model
                                                               October 26, 2004, 06:20:00
                                                                                                                                 1 PRGAPMWLRCVCQMLETKFL 20
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                             US-10-066-965A-4
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Sequence 4,
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                                          Sequence
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US-09-621-976-4938

Sequence 4938, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENERI C054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: 1876

SOFTWARE: Patent.pm

SOFTWARE: Patent.pm

LENGTH: 77
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PCT-US95-03718-4
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US-08-434-878-2
US-09-872-136B-2
PCT-US92-02750-2
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PCT-US92-09833-2
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US-08-122-517-4
US-08-122-517-4
US-07-906-397A-4
US-07-906-397A-4
US-09-021-324-4
US-09-021-324-4
US-08-434-878-4
US-08-434-878-4
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Best Local Similarity 77.8
Matches 7; Conservative
        489 PRGSPAWLR 497
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: 05/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59364
LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43959, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERBNCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION UMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
IENGTH: 239
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                         37.8%; Score 43.5; DB 4; Length 77; 53.3%; Pred. No. 7.8; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

37.4%; Score 43; DB 4; Length 154;

Best Local Similarity 47.4%; Pred. No. 19;

Matches 9; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.4%; Score 43; DB 4; Length 239; 47.4%; Pred. No. 31; tive 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-59364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                            US-09-270-767-59364
; Sequence 59364, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Drosophila melanogaster
                   ) LOCATION: 20
; OTHER INFORMATION: Xaa = Met, Arg
US-09-621-976-4938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PRGAPMWLRCVCOMLETKF 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 PRETPMSLECLXYYLXNKF
                                                                                                                                                                                         1 PRGAPMWLRCVCOML 15
                                                                                                                                                                                                                                2 PRSQPYW-RCCCNFL 15
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                                                                                                     Query Match
Best Local Similarity 53.33
Matches 8; Conservative
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Best Local Similarity
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-270-767-43959
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                                                                                                                                                                                                                                                                                             RESULT 3
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RESULT 5

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MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS
Sequence 7, Application US/09070356
| Patent No. 6228631
| GENERAL INFORMATION:
| APPLICANT: Alex Zhu
| APPLICANT: Jack Goldstein
| TITLE OF INVENTION: Recombinant a-N-
| TITLE OF INVENTION: Enzyme and cDNA Encoding
| TITLE OF INVENTION: Enzyme and cDNA Encoding
| TITLE OF INVENTION: Said Enzyme
| NUMBER OF SEQUENCES: 7
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: AMSTET, ROCHSTEIN & EDENSTEIN
| STREET: 90 Park Avenue
| CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: den Herder et al
TITLE: Cloning and Expression of a Member
TITLE: of the Aspergillus niger Gene Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Aspergillus niger a-galactosidase LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,248
FILING DATE: MARCH 26, 1993
ATTORNEY/ACENT INPORMATION:
NAME: PASQUALINI, PALTICIA A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: 63475/12
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 286-0854 or 286-0082
TELERA: (212) 286-0854 or 286-0082
TELERA: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/070,356 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS_DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Aspergillis niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGI, ... MOLBCULE TYPE: DESCRIPTION: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANELLE:
IMMEDIATE SOURCE: library
POSITION IN GENOME: unknown
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: doi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB TYPE:
CELL TYPE:
CELL LINE:
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APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: THOMAS P. LEARY
APPLICANT: THOMAS P. LEARY
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIKR
APPLICANT: SHERI L. BUIKR
APPLICANT: SHERI L. BUIKR
APPLICANT: SER K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
                                          Gaps
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37.4%; Score 43; DB 4; Length 1422; 36.0%; Pred. No. 2e+02; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D377/AP6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR PAPLICATION:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PORRMASKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
                                                                                                                          1262 PHXSPACKKVVIWLTCRCQWGQLKF 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5527.PC.01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Palace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/488,44
                                                                                     1 PRGAP-----MWLRCVCQMLETKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEB: ABBOTT LABORATORIES STREET: 100 ABBOTT PARK ROAD CITY: ABBOTT PARK
                                                                                                                                                                                                                          Sequence 86, Application US/08488446 Patent No. 6558898 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 86: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 1422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                            9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
      Query Match
Best Local Similarity
Matches 9; Conserva
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US-08-467-344A-86
                                                                                                                                                                                          RESULT 7
US-08-488-446-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANTHONY SCOTT MUBRHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                  ..
o
                                                                                                                                                                                                                    ouery Match
Best Local Similarity 42.1%; Pred. No. 60;
Matches 8; Conservative
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ZIP: 0.05A
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DE Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: ABBOTT LABORATORIES D377/AP6D
1: 100 ABBOTT PARK ROAD
ABBOTT PARK
              Encoding a-Galactosidase
Molecular and General Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5527.PC.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 86, Application US/08469260A Patent No. 6421578 GENERAL INFORMATION: APPLICANT: JOHN N. SIMONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAMSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
                                                                                                                                                            PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          1 PRGAPMWLRCVCQMLETKF 19
                                                                                                                                                                                                                                                                                                                                                               PMGPNNWARFMCDLNETLF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPONTUMICATION INFORMATION:
TELEPAX: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 86: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                          404-410
1992
                                                                                                DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
STREET: 100
CITY: ABBOT
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-469-260A-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-469-260A-86
                   TITLE: En
JOURNAL:
VOLUME: 2
PAGES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                       US-09-070-356-7
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Gaps

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Sequence 5158, Application US/09134001C

Sequence 5158, Application US/09134001C

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                            APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
CORRESPONDENCES: 716
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: 110
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                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
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                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 6064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435435
ATTORNEY FAGENT INFORMATION:
NAME: POREMESKT, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REPERRENCE/DOCKET NUMBER: 5527.PC
TELEPRONIUNICATION INFORMATION:
TELEPRONE: 708-937-6365
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1422 amino acids
                                                       JAMES C. ERKER
SHERI L. BUIJK
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Best Local Similarity 36.07
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Best Local Similarity
Matches 6; Conserv
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US-09-134-001C-5158
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                                                                             APPLICANT:
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                                                                                                                                                                                                                                     ANIBOLA COLLECTE STATES SHERE SHEET L. BUILTE I. BUILTE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDIUM TYPE: FLODPY disk
MEDIUM TYPE: FLODPY disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
CONTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-Jun-1995
CLASSIFCATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PRIOR APPLICATION NUMBER: 08/424,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.4%; Score 43; DB 4; Length 1422; Best Local Similarity 36.0%; Pred. No. 2e+02; Matches 9; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
; Sequence 86, Appl.
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT JOHN N. SIMONS
; GEORGE J. DAWSON
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEBARY
ANTHONY SCOTT MUERHOFF
"WAS C. ERKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
INFORMATION FOR SEQ ID NO: 86:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-08-467-344A-86
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Patent No. 6720166
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1422 amino acids
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ATTORNEY/AGENT INFORMATION:
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APPLICANT:
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APPLICANT:
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US-09-270-767-39796

Sequence 39796, Application US/09270767

Sequence 39796, Application US/09270767

Sequence 39796, Application US/09270767

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PACENTIN Ver. 2.0
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Fatent No. 6639063
FATENT No. 6639063
FAPPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dobert, S.
FILE REFERENT: Glockano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENT GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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Pred. No. 30;
0; Mismatches
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US-09-270-767-39796
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64;
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Pred. No. 18;
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Best Local Similarity 63.6%; Pred. No. (
Matches 7; Conservative 0; Mismatral
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                                                                                            ORGANISM: Pseudomonas aeruginosa
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1998-07-27
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Best Local Similarity 63...
7; Conservative
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Best Local Similarity
                   NUMBER OF SEQ ID NOS:
SEQ ID NO 22897
PRIOR FILING DATE:
                                                                                                                US-09-252-991A-22897
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US-09-621-976-7736
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LENGTH: 70
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                                                                               TYPE: PRT
                                                         LENGIH:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLILNG DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: FILE REFERENCE: 7126-094
CURRENT APPLICATION NUMBER: 05/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 53884
LENGTH: 91
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: 7326-034
CURRENT APPLICATION NUMBER: 05/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38667
LENGTH: 91
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Pred. No. 16;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     36.5%; Score 42; DB 4; Length 91; 75.0%; Pred. No. 16;
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                                                                                                                                      Sequence 38667, Application US/09270767 Patent No. 6703491
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US-09-270-767-53884
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         6 MWLRCVCQML 15
                                 26 MWINCVCCVL 35
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Best Local Similarity
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Matches 6; Conserv
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US-09-270-767-38667
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Search completed: October 26, 2004, 06:47:58 Job time: 23 secs

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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2328, 2001
Science 294, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                      A;Residues: 1-518 <KUR>
A;Cross-references: UNIPROT:Q8UDI2; GB:AE007869; PIDN:AAK87890.1; PID:g15157282; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Vng2064h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: C84356
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, W.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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A;Cross-references: UNIPROT:Q9HNK5; GB:AE004437; NID:g10581482; PIDN:AAG20215.1; GSPDB:G
C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, 9, 2001
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Cipate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
Cipate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
Cipate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
Riottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: 223031
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A,Experimental source: adult testis; clone DKFZp434M0519
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein DKFZp434M0519.1 - human (fragment)
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100.0%; Pred. No. 0.2
tive 0; Mismatches
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100.0%; Pred. No. 3;
live 0; Mismatches
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100.0%; Pred. No. 14;
tive 0; Mismatches
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A, Map position: circular chromosome
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                            A;Accession: A97617
A;Status: preliminary
A;Molecule type: DNA
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Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A; Reference number: A82950; MUD:2043737; PMID:10984043

A; Recession: C83311

A; Accession: C83312

A; Residues: 1-297 <STO>
A; Residues: 1-207 <STO
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-504 <KUR>
A;Residues: 1-504 <KUR>
A;Zross-references: UNIPROT:Q8UDI2; GB:AE008688; PIDN:AAL43133.1; PID:g17740607; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG2839
hypothetical protein Atu2143 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG2839
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probable transport protein (PA4023) [imported] - Agrobacterium tumefaciens (strain C58, probable transport protein tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97617
C;Accession: A97617
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; FMID:11743193
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                                                                                                                                                                         hypothetical protein PA2661 [imported] - Pseudomonas aeruginosa (strain PA01)
                                                                                                                                                                                                      Species: Pseudomonas aeruginosa
Date: 15-8ep-2000 #sequence_revision 15-8ep-2000 #text_change 09-Jul-2004
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A, Map position: circular chromosome
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Best Local Similarity
Matches 8; Conserv
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A; Status: preliminary
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Tue Oct 26 08:02:13 2004

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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoç
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q311W1; GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05547.
A;Experimental source: strain PAO1
                                                                                                                                                                                                                             conserved hypothetical protein PA2154 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Species: Xanthomonas campestris
C;Species: Xanthomonas campestris
C;Species: Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S67856
R;Pollock, T.J.
submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83377
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C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Jul-2004
C,Accession: JN0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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. 26;
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100.0%; Pred. No. 24;
tive 0; Mismatches
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100.0%; Pred. No. 26;
iive 0; Mismatches
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Best Local Similarity 100.0
Local 6; Conservative
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                                                          254 WRWLRR 259
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-361 <CRI>
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10 WRWLRR 15
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A; Residues: 1-331 <STO>
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                                                                                                                                                                                                        Particle protein XF1099 [imported] - Xylella fastidiosa (strain 9a5c)
C,Species: Xylella fastidiosa
C,Species: The Xylella fastidiosa
S,Itale: The Sylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A,Itale: The genome Sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: A88515; MUD:20365717; PMID:10910347
A,Note: for a complete list of authors see reference number A59328 below
A,Scession: F62725
A,Recioule type: DNA
A,Recioule type: DNA
A,Residue: 1-191 <SINA
A,Residue: 1-191 <SINA
A,Residue: The XSINA
A,Resi
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83210
C;Accession: D83210
R;Stover C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
", Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A92950; MUID: 20437337; PMID: 10984043
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A,Experimental source: strain PAO1
C,Genetics:
A,Gene: PA3483
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100.0%; Pred. No. 16;
:ive 0; Mismatches
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Best Local Similarity
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100.0%; Pred. No. 29;
tive 0; Mismatches
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100.0%; Pred. No. 33;
ive 0; Mismatches
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                                           106 SLWALG 111
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Matches 6; Conserv
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A; Residues: 1-52 <SCF>
  SLWALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           introns: 62/1; 89/3
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87644
R;Nierman, W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87644
A;Accession: F87644
A;Accession: P87644
A;Accession: P87644
A;Accession: P87644
A;Accession: R97644
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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J. Lory, S.; Olson, M.V.

Mature 406, 959-964, 2000

A.Aitle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A.Reference number: A82950; MUID:20437337; PMID:10984043

A.Reference number: A82950; MUID:20437337; PMID:10984043

A.Residues: preliminary

A.Molecule type: DNA

A.Residues: 1-426 <STO>
A.Residues: 1-426 <STO>
A.Residues: Laro Complete Strain PA01

A.Residues: Laro Complete Strain PA01

A.Gross-references: UNIPROT:Q9HYD1; GB:AE004768; GB:AE004091; NID:g9949611; PIDN:AAG0686
                A Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Crossidues: 1-379 < POL>
A; Cross-references: UNIPROT:Q56773; EMBL:U22511; NID:g1172090; PIDN:AAA86375.1; PID:g733
C; Genetics:
A; Gene: gumG
C; Superfamily: O-acetyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rhamnosyltransferase chain B PA3478 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Date: 15-8ep-2000 #sequence_revision 15-8ep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 28;
iive 0; Mismatches
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30.0%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches
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C;Superfamily: glycosyltransferase
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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A;Accession: S67856
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C;Accession: B53652
R;Ochsner, U.A.; Fiechter, A.; Reiser, J.
Biol. Chem. 269, 19787-19795, 1994
A;Title: Isolation, characterization, and expression in Escherichia coli of the Pseudomo A;Reference number: A53652; MUID:94327521; PMID:8051059
                                                                                                                                                                                                                                                                                                                   A, Status: preliminary
A, Molecule type: DNA
A, Fesidues: 1-426 <OCH>
A, Cross-references: UNIPROT: Q51560; GB: L28170; NID: g452502; PIDN: AAA62129.1; PID: g452504
C, Superfamily: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1495 <SCH>
A;Cross-references: UNIPROT:P46882; EMBL:L38858; NID:g619754; PIDN:AAA98490.1; PID:g6197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 165-175 <670v>
R;Robilling, B.; Lerch, K.
Biochim. Biophys. Acta 1243, 529-537, 1995
A;Title: Anine oxidases from Aspergillus niger: identification of a novel flavin-depende
A;Reference number: $60356; MUID:95244610; PMID:7727530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S55273; S55267; S60356
R;Schilling, B.; Lerch, K.
Mol. Gen. Genet. 247, 430-438, 1995
A;Title: Cloning, sequencing and heterologous expression of the monoamine oxidase gene A;Reference number: S55267; MUID:95287865; PMID:7770050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence not shown; not compared with conceptual translation
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                         C;Species: Pseudomonas aeruginosa
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: monoamine oxidase N
C;Species: Aspergillus niger
C;Date: 14-Oct-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
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F;41-69/Region: beta-alpha-beta FAD nucleotide-binding fold
F;493-495/Region: peroxisome/glyoxysome location signal #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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rhamnosyltransferase 1 chain B - Pseudomonas aeruginosa
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Cispecies: Homo sapiens (man)—
Cispecies: Homo sapiens (man)—
Cibate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
Cibate: 05-Mar-1099 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
Cibate: 05-Mar-10245
Rilamerdin, J.E.; McGready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, K.; Gc.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, T.; Trankhein submitted to the RNEL Data Library, March 1998
A;Authors: Duarte, S.; Lucas, S.; Bruce, R.; Thomas, P.; Quan, G.; Kronmiller, B.; Arelle A;Description: Sequence analysis of a human P1 clone containing the XRCC9 DNA repair gene A;Reference number: Z14637
A;Accession: T02245
A;Accession: T02245
A;Molecule type: DNA
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A;Notes: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg A;Notes: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: F88559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76730
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-636 - KRN>
A;Cross-references: UNIPROT:P74536; EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA1864;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                  C;Species: Synethocystis sp.
C;Species: Synethocystis sp.
C;Species: Synethocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accesion: 376730
R;Raneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
R;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, A.; Kse. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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A;Map position: 9
A;Introns: 89/3; 152/1; 200/1; 241/2; 294/3; 354/3; 435/1; 733/1; 802/1; 871/1
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A;Cross-references: EMBL:AC004472; NID:g2984582; PIDN:AAC07985.1; PID:g2984587
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004
C;Accession: F88559
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100.0%; Pred. No. 40;
iive 0; Mismatches 0; Indels
                                                                                          Synechocystis sp. (strain PCC 6803)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Score 6; DB 2;
ilarity 100.0%; Pred. No. 51;
Conservative 0; Mismatches
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Best Local Similarity
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                                                                                                          hypothetical protein
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                                RESULT 17
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probable membrane protein YBR220c - yeast (Saccharomyces cerevisiae)

probable membranes: hypothetical protein YBR1510

C;Species: Saccharomyces cerevisiae

C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C;Accession: S46096

R;Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;

submitted to the Protein Sequence Database, August 1994

A;Reference number: S45782

A;Reference number: S45782

A;References: UNDA

A;Residues: 1-560 cDUB

A;Cross-references: UNIPROT:P38318; EMBL:Z36088; NID:g536609; PID:g536611; GSPDB:GN00002

A;Gnetics:
A;Gnetics: A;Gnetics: SGD:S0000424
process Arabidopsis thaliana (mouse-ear cress)
C; Becies: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: E8625 thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: E8626 than the common than the common that change of the change of the change of the common that change of the chang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 522;
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C:Keywords: transmembrane protein
F;18-37/Domain: transmembrane #status predicted <TM01>
F;88-106/Domain: transmembrane #status predicted <TM02>
F;139-155/Domain: transmembrane #status predicted <TM03>
F;177-193/Domain: transmembrane #status predicted <TM04>
F;218-238/Domain: transmembrane #status predicted <TM04>
F;218-238/Domain: transmembrane #status predicted <TM05>
F;330-347/Domain: transmembrane #status predicted <TM05>
F;491-407/Domain: transmembrane #status predicted <TM07>
F;421-477/Domain: transmembrane #status predicted <TM09>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Conservative 0; Mismatches
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100.0%; Pred. No. 34;
iive 0; Mismatches
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hes 6, Conserv
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A;Molecule type: DNA
A;Residues: 1-522 <STO>
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Length 60;

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A;Map position: 86.78-87.15
A;Start codon: GTG
C;Superfamily: phage lambda hypothetical 7.4K protein (nin region)
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                                                                                                                                                                                                                                                             5; Conservative
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Matches 5; Conserv
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                        C;Genetics:
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D83827
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Rikershaw, J.

submitted to the EMBL Data Library, November 1995

A;Reference number: S60124

A;Reference number: S60124

A;Molecule type: DNA

A;Residues: 1-1767 «KER»

A;Cross-references: EMBL: Z29117; NID: 9439247; PID: 91066912

C;Genetics:
A;Map position: III

A;Introns: 47/1; 112/3; 161/2; 220/2; 543/3; 574/3; 903/2; 1056/1; 1115/3; 1178/3; 1265/
C;Genetics:
A;Map position: III

A;Introns: 47/1; 112/3; 161/2; 220/2; 543/3; 574/3; 903/2; 1056/1; 1115/3; 1178/3; 1265/
C;Geywords: ATP: duplication; nucleotide binding motif A (P-loop)

F;648-652/Region: mucleotide-binding motif B (P-loop)

F;64769/Region: mucleotide-binding motif B

F;1457-1642/Domain: ATP-binding cassette homology <ABCC>
F;1457-1642/Domain: ATP-binding motif B

F;1586-1591/Region: nucleotide-binding motif B

F;1586-1591/Region: nucleotide-binding motif B
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(XBP7L
hypothetical protein C-60 (nin region) - phage lambda
C;Species: phage lambda
C;Species: phage lambda
C;Date: 13-Jun-1983 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: C43011; H43016; Ä04393
R;Daniels, D.
submitted to the Nucleic Acid Sequence Database, September 1982
R;Accession: C43011
A;Recence number: A94614
A;Recession: C43011
A;Recence: UNIPROT:P03768
R;Sanger, F; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
A;Reference number: A92891; MUID:83189071; PMID:6221115
A;Recence number: A92891; MUID:83189071; PMID:6221115
A;Recoule type: DNA
A;Reference number: A92891; MUID:83189071; PMID:6221115
A;Recoule type: DNA
A;Residues: 1-60 <AN>
A;Residues: 1-60 <AN
A;Residues: 1-60
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1758 <STO>
A;Cross-references: GB:chr_III; PIDN:CAA82384.1; PID:g3875025; GSPDB:GN00021; CESP:C48B4
C;Generics:
C;Generics:
A;Map Position: 3
C;Superfamily: ATP-binding cassette homology
C;Superfamily: ATP-binding cassette homology
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C;Species: Caenorhabditis elegans
C;Date: 13-Jan.1996 #sequence revision 12-Apr-1996 #text_change 16-Aug-2004
C;Accession: S60124; S40724; S40725
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                                                                                                                                                                                                                                                                                                              30.0%; Score 6; DB 2
100.0%; Pred. No. 87;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
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Best Local Similarity
Matches 6; Conserva
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Na+/H+ antiporter nahS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Datilus halodurans
C;Date: 0.1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: DB3827
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule,type: DNA
A;Residues: 1-65 <STO>
A;Cross-references: UNIPROT:Q9KCZ9; GB:AP001512; GB:BA00004; NID:g10174030; PIDN:BAB051
A;Experimental source: strain C-125
C;Genetics:
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A7273
B;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KNA Res. Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MulD:99310339; PMID:10382966
A;Accession: A7273
A;Acce
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25.0%; Score 5; DB 1;
100.0%; Pred. No. 78;
tive 0; Mismatches
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100.0%; Pred. No. 83;
cive 0; Mismatches
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100.0%; Pred. No. 93;
iive 0; Mismatches
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C;Accession: I59068
R;Geliebter, J.; Zeff, R.A.; Melvold, R.W.; Nathenson, S.G.
Proc. Natl. Acad. Sci. U.S.A. 83, 3371-3375, 1986
A;Title: Mitotic recombination in germ cells generated two major histocompatibility compl
A;Reference number: I59068; MUID:86205899; PMID:3458188
A;Accession: I59068
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R;Thomas, W.K.; Beckenbach, A.T.
Nol. 29, 233-245, 1989
A;Title: Variation in salmonid mitochondrial DNA: evolutionary constraints and mechanisms A;Reference number: A30396; MUID:89382658; PMID:2550657
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MDH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) Chain 4L - cutthroat trout mitochondrion (1
C;Species: mitochondrion Salmo clarki (cutthroat trout)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.H.; Mellor, A.L.; Flave
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1.91 <RES>
A;Cross-references: UNIPROT:Q95555; GB:M12935; NID:q199595; PIDN:AAA39677.1; PID:q554238
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC K-bm6 transplantation antigen - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 157611
R;Geliebter, J:; Zeff, R.A.; Schulze, D.H.; Pease, L.R.; Weiss, E.H.; Mellor, A.L.;
Mol. Cell. Biol. 6, 645-652, 1986
A;Title: Interaction between K-b and Q4 gene sequences generates the K-bm6 mutation. A;Reference number: 157611, MUID: 87064350; PMID: 3023861
A;Accession: 157611
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                                                   Length 91;
                                                                                             1.1e+02;
hes 0;
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A;Molecule type: mRNA
A;Residues: 1-91 <RES>
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A,Molecule type: DNA
                                                        DB 2;
                                                   25.0%; Score 5; DB 2
100.0%; Pred. No. 1.1
cive 0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
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les 5; Conservative
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                                                   Query Match
Best Local Similarity
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Best Local S:
Matches 5
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I57611
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 156009
R;Sire, J; Chimini, G; Boretto, J; Toubert, A.; Kahn-Perles, B.; Layet, C.; Sodoyer, J; Chimini, G; Boretto, J; Toubert, A.; Kahn-Perles, B.; Layet, C.; Sodoyer, J; Timunol. 140, 2422-2430, 1988
A;Title: Hybrid genes between HLA-A2 and HLA-A3 constructed by in vivo recombination all A;Reference number: 156009; MUID:88170828; PMID:2450922
A;Accession: 156009
A;Refarence number: 156009; MUID:88170828; PMID:2450922
A;Accession: 156009
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-89 cRES>
A;Cross-references: UNIPROT:Q30176; GB:M20139; NID:g188493; PIDN:AAA59838.1; PID:g553587
C;Genetics:
A;Genetics:
A;Ge
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A;Title: comparison of the cloned h-2kbml variant gene with the h-2kb gene shows a clust A;Reference number: 158989; MUID:83169810; PMID:6300887
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A;Cross-references: UNIPROT:Q31190; GB:J00401; NID:g199540; PIDN:AAA39651.1; PID:g554232
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q49621; EMBL:U00010; NID:g466780; PIDN:AAA17064.1; PID:g4667
C;Genetics:
A;Gene: kas
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probable ketoacyl synthase kas - Mycobacterium leprae
N;Alternate names: Lepbl170_C1_189 protein
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72700
R;Smith, D.R.; Robison, K.
submitted to the RMLD Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1170.
A;Reference number: S72693
A;Accession: S72700
A;Status: preliminary
A;Residues: 1-84
A;Malecule type: DNA
A;Ma
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A,Molecule type: DNA
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Matches
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Tue Oct 26 08:02:13 2004

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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - sockeye salmon mitochondrion (f
                                                                                                                                                                                                                                                                                                                C;Species: mitochondrion Oncorbynchus nerka (sockeye salmon)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: F30401
C;Accession: F30401
C;Accession: E30401
A;Accession: F30401
C;Accession: F30401
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C;Accession: F30401
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C;Species: mitochondrion Oncorhynchus tschawytscha (chinook salmon)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: 630401
R;Thomas, W.K.; Beckenbach, A.T.
A;Tile: Variation in salmonid mitochondrial DNA: evolutionary constraints and mechanism A;Reference number: A30396; MUID:89382658; PMID:2550657
A;Accession: G30401
A;Accession: G30401
A;Accession: preliminary; not compared with conceptual translation
A;Residues: 1-92 cTHO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Genome: mitochondrion
A,Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Genome: mitochondrion
A,Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; oxidative phosphorylation;
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                         Indels
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                      Mismatches
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A, Cross-references: UNIPROT:P11630
C, Genetics:
                  5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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                  Matches
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NADA2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - coho salmon mitochondrion (frag C;Species: mitochondrion Oncorhynchus kisutch (coho salmon)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: B30401
R;Thomas, W.K.; Beckenbach, A.T.
J. Mol. Evol. 29, 233-245, 1989
A;Title: Variation in salmonid mitochondrial DNA: evolutionary constraints and mechanism A;Reference number: A30396; MUID:89382658; PMID:2550657
A;Accession: B30401
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Stesidues: 1-92 <THO>
A;Cross-references: UNIPROT:P11630
C;Genetics:
A;Geneme: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
A; Accession: H30401
A; Status: preliminary; not compared with conceptual translation
A; Status: preliminary; not compared with conceptual translation
A; Status: 1-92 < THD>
A; Cross-references: UNIPROT: P11630
C; Genetics:
A; Genetics:
A; Genetic code: SGC1
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C; Superfamily: NADH dehydrogenase (upiquinone) chain 50 cxidative phosphorylation;
C; Seywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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C;Species: mitochondrion Oncorhynchus gorbuscha (pink salmon)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: D30401
R;Thomas, W.K.; Beckenbach, A.T.
J. Mol. Bvol. 29, 233-245, 1989
A;Title: Variation in salmonid mitochondrial DNA: evolutionary constraints and mechanism A;Reference number: A30396; MUID: 89382658; PMID: 2550657
A;Accession: D30401
A;Accession: D30401
A;Accession: D30401
A;Molecule type: DNA
A;Residues: 1-92 <THO>
A;Residues: 1-92 <THO>
C;Genetics:
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A)Genetic code: SGC1
C)Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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                                                                                                                                                                                                                                                                                                                                      Query Match 25.0%; Score 5; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
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Query Match Best Local Similarity 100. Matches 5; Conservative

44 SLWAL 48

RESULT 35

4 SLWAL 8

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A.Genome: mitochondrion
A.Genetic code: SGC1
C.Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C.Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C.Keywords: electron transfer; membrane-associated complex; mitochondrion; NAD; oxidative
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - Atlantic salmon mitochondrion C;Species: mitochondrion Salmo salar (Atlantic salmon)
C;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 09-Uul-2004
C;Accession: T09959:
Submitted to Lhe EMBL Data Library, October 1998
A;Reference number: Z16904
A;Reference number: Z16904
A;Accession: T09955
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C;Species: Samia cynthia (ailanthus silkmoth)
C;Pecies: Samia cynthia (ailanthus silkmoth)
C;Accession: JQ0906
R;Iwami, M.
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C;Species: Samia cynthia (ailanthus silkmoth)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-98 <HUR>
A;Cross-references: UNIPROT:Q92ZM5; EMBL:U12143; NID:g3775976; PID:g3776543
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A;Residues: 1-98 <IWA>
A;Cross-references: UNIPROT:P33720
A;Note: the authors translated the codon ATA for residue 32 as Thr
A;Note: the source is designated as Samia cynthia ricini
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A;Residues: 1-99 <IMA>
A;Cross-references: UNIPROT:P33718
A;Cross-the source is designated as Samia cynthia ricini
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. 1.1e+02;
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100.0%; Pred. No. 1.1
tive 0; Mismatches
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A;Reference number: JQ0902
A;Accession: JQ0906
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A;Reference number: JQ0902
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Best Local Similarity 100.
Matches 5; Conservative
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C;Species: mitochondrion Oncorhynchus mykiss (rainbow trout)
C;Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text_change 09-Jul-2004
C;Datesion: T09865; J30401; S04689
R;Zardosy, R; Garrido-Pertierra, A.; Bautista, J.M.
J. Mol. Bvol. 41, 942-951, 1995
A;Title: The complete nucleotide sequence of the mitochondrial DNA genome of the rainbow A;Reference number: Z16890; MUID:96139027; PMID:8587139
A;Accession: T09865
A;Accession: T09865
A;Moleçule type: DNA
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R, Thomas, W.K.; Beckenbach, A.T.
D, Mol. Brol. 29, 233-245, 1989
A, Title: Variation in salmonid mitochondrial DNA: evolutionary constraints and mechanism A, Reference number: A30396; MUID:89382658; PMID:2550657
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A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-92 < THG>
R, Davidson, W.S.; Bartlett, S.E.; Birt, T.P.; Green, J.M.
Curr. Genet. 14, 483-486, 198
A; Title: Cloning and sequence analysis of an Xbal fragment of rainbow trout mitochondria
A, Reference number: S04688; MUID:89136066; PMID:3265651
                       R,Venanzetti, F.; Cecconi, F.; Giorgi, M.; Cesaroni, D.; Sbordoni, V.; Mariottini, P. Curr. Genet. 26, 139-145, 1994
A;Title: Cloning and characterization of the European seabass, Dicentrarchus labrax, mit A;Reference number: S45489; MUD:95094310; PMID:8001168
A;Accession: A54549
A;Molecule type: DNA
A;Residues: 1-97 <VEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-98 <ZAR>
A;Cross-references: UNIPROT:P11630; EMBL:L29771; NID:g1246865; PIDN:AAB03355.1; PID:g463
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A,Genome: mitochondrion
A,Genetic SGC1
C,Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C,Superfamily: NADH dehydrogenase (ubiquinone) chain 8L
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q36364; EMBL:X74148; NID:g521080; PIDN:CRA52245.1; PID:g521d
C;Genetics:
                                                                                                                                                                                                                                                                                                                        A;Genome: mitochondrion
A;Genteic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A;Residues: 1-2,'ALWHQYTSA',8-25,'FS',28,'P',30-35 <DAV>
A;Cross-references: EMBL:X14013; NID:g13622; PIDN:CAA32179.1; PID:g13624
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.0%; Score 5; DB 2; Length 97; 100.0%; Pred. No. 1.1e+02; Live 0; Mismatches 0; Indels
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A;Accession: C30401 A;Status: preliminar

A; Accession: S04689

5; Conservative

SLWAL 49

RESULT 36 T09955

4 SLWAL 8

Query Match Best Local Similarity

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CiSpecies: Definococcus radiodurans
CiSpecies: Definococcus radiodurans
CiDate: 0.3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
CiAccession: H75591
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamarhevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-116 <WHI>
A;Cross-references: UNIPROT:Q9RYF3; GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF1250
A;Experimental source: strain R1
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C. Accession: H72489
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C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 11-Jan-2000
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 11-Jan-2000
C;Accession: S51207
R;Tateno, M.; Ihara, K.; Mukohata, Y.
Arch. Biochem. Biophys. 315, 127-132, 1994
A;Title: The novel ion pump rhodopsins from Haloarcula form a family independent from bot
                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A,Reference number: A75250; MUID:20036896; PMID:10567266
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C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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C;Superfamily: Deinococcus radiodurans hypothetical protein DRA0365
                                                                                                                                                                     hypothetical protein DRA0365 - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cruxhalorhodopsin-1 - Haloarcula sp. (fragment)
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-116 <KAW>
               54
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A;Molecule type: DNA
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hypothetical protein SA1825 [imported] - Staphylococcus aureus (strain N315)

C; Species: Staphylococcus aureus

C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Uul-2004

C; Accession: H89992

R; Kuroda, M; Ohta, T; Uchiyama, I.; Baba, T; Yuzawa, H; Kobayashi, I;; Cui, L; Ogud

R; Kuroda, M; Ohta, T; Hattori, M; Gayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, K;

C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.

Ci; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A; Reference number: A89758; MUID:21311952; PMID:11418146

A; Accession: H89992

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-113 < KUR>

A; Consorreferences: UNIPROT:0998M8; GB:BA000018; PID:g13701812; PIDN:BAB43105.1; GSPDB:G

C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
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C; Species: Listeria monocytogenes
C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C; Accession: Ad1237
C; Dominguez-Bernal, G; Duchaud, E; Durand, L; Dussurget, O; Entian, K.D.; Fsihl, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G; Madueno, E.; Maitcournam, A.; Maok, C.; Schlucter, T.; Simoces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Residues: 1-109 cGLAb
A; Residues: 1-109 cGLAb
A; Cross-references: UNIPROT:Q877H6; GB:NC_003210; FIDN:CAC99381.1; PID:g16410719; GSPDB: A; Experimental source: strain EGD-e
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25.0%; Score 5; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 5; Conservative
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C,Genetics:
A,Gene: sbxAl
C,Superfamily: insulin
C,Keywords: hormone
                                                                                                                                                                                                                                                                               9 GWRWL 13
                                                                                                                                                                                                                                                                                                                                     59 GWRWL 63
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A; Reference number: S51206; MUID:95070153; PMID:7979388

A;Experimental source: strain arg-1 C;Superfamily: bacteriorhodopsin C;Keywords: chromoprotein; photoreceptor; retinal; transmembrane protein

A;Residues: 1-118 <TAT>

A; Accession: S51207 A; Molecule type: DNA

0

25.0%; Score 5; DB 2; Length 118; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels

Query Match 25.0 Best Local Similarity 100. Matches 5, Conservative

90 LWALG 94

5 LWALG 9

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"Nighternate names: protein F8B4.170
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 27-Oct-2003
C;Accession: T05357,
C;Accession: T05357,
C;Accession: T05357,
C;Accession: T05357,
C;Accession: T05357,
C;Accession: T05357,
C;Accession: Soquence_revision can be be be believed.
C;Accession: Description can be believed.
C;A
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A;Note: F884-170
C;Superfamily: ubiquinol-cytochrome-c reductase 14 kDa protein
C;Keywords: electron transfer; membrane protein; membrane-associated complex; mitochondri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytochrome-c oxidase (EC 1.9.3.1) chain I - pocket gopher (Geomys breviceps) mitochondric c; Species: mitochondrion Geomys breviceps (pocket gopher) (;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004 (;Accession: 163123 F;Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler, Science 265, 1087-1090, 1994 Mittle: Disparate rates of molecular evolution in cospeciating hosts and parasites.
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A;Molecule type: DNA
A;Residues: 1-125 <CRU>A;Residues: UNIPROT:080152; EMBL:AF009630; NID:g3282260; PIDN:AAC27230.1; PID:g32
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R;Crutz-Le Coq, Am.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, M. submitted to the EMBL Data Library, June 1997

A,Description: Sequence and organization of the lactococcal isometric bIL170 phage genome
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C,Species: Lactococcus phage bIL170
C,Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Cross-references: EMBL:AL034567
A;Experimental source: cultivar Columbia; BAC clone F8B4
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C,Superfamily: Lactococcus phage bIL170 gene e8 protein
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Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity 100.C
Matches 5; Conservative
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A, Accession: T05357
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A; Accession: T03359
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A;Cross-references: UNIPROT:059124; GB:AP000006; NID:g3236133; PIDN:BAA30562.1; PID:g325
A;Cross-references: UNIPROT:059124; GB:AP000006; NID:g3236133; PIDN:BAA30562.1; PID:g325
A;Experimental source: strain 0T3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1455
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A,Experimental source: Clostridium acetobutylicum ATCC624
C,Genetics
A,Gene: CAC1187
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hypothetical protein PH1455 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: B71020
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000, MUID:98344137; PMID:9679194
A;Accession: B71020
A;Accession: B71020
A;Accession: D71020
A;Anoleule type: DNA
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25.0%; Score 5; DB 2; Length 118; 100.0%; Pred. No. 1.3e+02; Live 0; Mismatches 0; Indels

5; Conservative

13 LRRYG 17 LRRYG 17

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13

Best_Local Similarity Matches 5; Conserv

Query Match

A; Residues: 1-118 < KUR>

A,Accession: D97046 A,Status: preliminary A,Molecule type: DNA

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25.0%; Score 5; DB 2; Length 120; ilarity 100.0%; Pred. No. 1.3e+02; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 5; Conserv

Tue Oct 26

Query Match 25.0%; Score 5; DB 2; Length 126; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels

98 LWALG 102

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5 LWALG 9

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cytochrome-c oxidase (BC 1.9.3.1) chain I - western pocket gopher (Thomomys bottae) mito
C;Species: mitochondrion Thomomys bottae (western pocket gopher)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: 163121
R;Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler Science 265, 1087-1099, 1994
A;Hitle: Disparate rates of molecular evolution in cospeciating hosts and parasites. A;Reference number: 148088; MUID:94345374; PMID:8066445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-126 <RES>
A/Cross-references: UNIPROT:Q36004; GB:L32682; NID:g548217; PIDN:AAA66277.1; PID:g548218
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A,Genetic code: SGC1
C,Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C,Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopro
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A;Cross-references: UNIPROT:Q34642; GB:L32689; NID:g548227; PIDN:AAA66281.1; PID:g548228
C;Genetics:
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C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopro
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C;Species: mitochondrion Thomomys talpoides (western pocket gopher)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
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A;Accession: 163125
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                                    red. No. 1.4e+02;
Mismatches 0;
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                          Best Local Similarity
Matches 5; Conserv
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A;Genetic code: SGC1
C;Superfamily: cytochrom
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Best Local Similarity
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C;Species: mitochondrion Cratogeomys merriami (pocket gopher)
C;Date: 04-180.89
C;Accession: 1480.89
R;Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler Science 265, 1087-1090, 1994
A;Title: Disparate rates of molecular evolution in cospeciating hosts and parasites.
A;Reference number: 1480.89
A;Reference number: 1480.89
A;Accession: 1480.89
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A;Accession: 1480.89
A;Residues; Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-126 <-RES
A;Cross-references: UNIPROT:Q34162; GB:L32688; NID:g548110; PIDN:AAA66244.1; PID:g548111
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: cytochrome-c oxidase chain 1; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex, metallopi
A;Reference number: 148088; MUID:94345374; PMID:8066445
A;Accession: 163123
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-126 <RES>
A;Cross_references: UNIPROT:Q34550; GB:L32683; NID:g548223; PIDN:AAA66279.1; PID:g548224
A;Genetics: mitochondrion
A;Genetic code: SGC1
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopi
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Cytochrome-c oxidase (EC 1.9.3.1) chain I - pocket gopher (Cratogeomys bulleri) mitochon C; Species: mitochondrion Cratogeomys bulleri (pocket gopher)

C; Species: mitochondrion Cratogeomys bulleri (pocket gopher)

C; Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

C; Accession: 163124

R; Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler A; File: Disparate rates of molecular evolution in cospeciating hosts and parasites.
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25.0%; Score 5; DB 2; Length 126; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100..

98 LWALG 102

5 LWALG 9

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A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopt
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

A; Residues: 1-126 < RES>

C; Genetics:

25.0%; Score 5; DB 2; Length 126;

Query Match

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RESULT 58
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C; Species: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C; Accession: IG3116
C; Accession: IG3116
A; Title: Disparate rates of molecular evolution in cospeciating hosts and parasites.
A; Reference number: 148088; MUID:94345374; PMID:8066445
A; Accession: IG3116
A; Accession: IG3116
A; Accession: IG3116
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-126 < RES>
A; Residues: 1-126 < RES>
C; Genetics:
   RiHafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler Science 265, 1087-1090, 1994
A; Title: Disparate rates of molecular evolution in cospeciating hosts and parasites.
A; Reference number: 148088; MUID:94345374; PMID:8066445
A; A; Accession: 163122
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-126 < RES>
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C;Species: mitochondrion Orthogeomys cherriei (pocket gopher)
C;Date: 04-Sep_1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
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A;Cross-references: UNIPROT:Q35241; GB:L32687; NID:g548199; PIDN:AAA66273.1; PID:g548200
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A)Genetic code: SGC1
C,Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopz
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                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q36172; UNIPROT:Q8M605; UNIPROT:Q8M601; GB:L32690; NID:g5482
                                                                                                                                                                                                                                                                                                                                                     A,Genome: mitochondrion
A,Genetic code: SGCI
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopr
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R;Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Na Science 265, 1087-1090, 1994
A;Title: Disparate rates of molecular evolution in cospeciating hosts and parasites.
A;Reference number: 148088; MUID:94345374; PMID:8066445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.0%; Score 5; DB 2; Length 126; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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C; Accession: I63122
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Matches
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A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome-c oxidase (EC 1.9.3.1) chain I - pocket gopher (Orthogeomys heterodus) mitochrosses: mitochondrion Orthogeomys heterodus (pocket gopher)
C;Dete: 04-5ep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I63120
R;Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q35257; GB:L32696; NID:g548205; PIDN:AAA66276.1; PID:g548206 C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology C;Superfamily: cytochrome-c magnesium; membrane-associated complex; metalloprometallopromes complex; electron transfer; magnesium; membrane-associated complex; metalloprometallopromes
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C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopro
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C;Genetics:
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A;Accession: 163119
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 265, 1087-1090, 1994
A;Title: Disparate rates of molecular evolution in cospeciating hosts and parasites. A;Reference number: 148088; MUID:94345374; PMID:8066445
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                                                                                                                   25.0%; Score 5; DB 2; Length 126;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-126 <RES>
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Matches 5; Conserv
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A,Cross-references: UNIPROT:Q34548; GB:L32693; NID:g548229; PIDN:AAA66282.1; PID:g54823C
                                            C;Genetics:
A;Genome: mitochondrion
A;Genome: mitochondrion
C;Supertic code: SGC1
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopr
                                                                                                                                                                                                                                                                                                                                             h Similarity 100.0%; Score 5; DB 2; Length 126; Similarity 100.0%; Pred. No. 1.4e+02; 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
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              Cytochrome-c oxidase (EC 1.9.3.1) chain I - pocket gopher (Orthogeomys underwood)) mitod CiSpecies: mitochondrion Orthogeomys underwood) (pocket gopher)
CiSpecies: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
CiAccession: 163118
R;Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler Science 265, 1087-1090, 1994
A;Thle: Disparate rates of molecular evolution in cospeciating hosts and parasites.
A;Reference number: 148088; MUID:94345374; PMID:8066445
A;Reference number: 148088; MUID:94345374; PMID:8066445
A;Residue: Disparate rates of molecular evolution in cospeciating hosts and parasites.
A;Residue: L126 <RES>
A;Residues: 1-126 <RES>
A;Residues: 1-126 <RES>
A;Genetics:
A;Genetics:
A;Genetic code: SGC1
C;Sepectamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopr
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Vytochrome-c oxidase (EC 1.9.3.1) chain I - pocket gopher (Geomys bursarius) mitochondri
C;Species: mitochondrion Geomys bursarius (pocket gopher)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: 163126
B;Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler
Science 265, 1087-1090, 1994
A;Title: Disparate rates of molecular evolution in cospeciating hosts and parasites.
A;Reference number: 148088; MUID:94345374; PMID:8066445
A;Accession: 163126
A;Accession: L63126
A;Accession: L631
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Best Local Similarity 100.00
Thes 5; Conservative
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cytochrome-c oxidase (EC 1.9.3.1) chain I - pocket gopher (Geomys bursarius) mitochondric C; Species: mitochondrion Geomys bursarius (pocket gopher)
C; Species: mitochondrion Geomys bursarius (pocket gopher)
C; Accession: IG3127
R; Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler A; Fine E 265, 1087-1090, 1994
A; Title: Disparate rates of molecular evolution in cospeciating hosts and parasites.
A; Reference number: I48088; MUID:94345374; PMID:8066445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-126 <RES>
A;Cross-references: UNIPROT:Q34549; GB:L32694; NID:g548231; PIDN:AAA66283.1; PID:g548232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopr
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C; Date: 0.46-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C; Accession: 148088
R; Hafner, M.S.; Sudman, P.D.; Villablanca, F.X.; Spradling, T.A.; Demastes, J.W.; Nadler, Science 265, 1087-1090, 1994
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A;Genetic code: SGCI
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metallopro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Disparate rates of molecular evolution in cospeciating hosts and parasites. A,Reference number: 148088; MUID:94345374; PMID:8066445
A,Accession: 148088
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-126 <RES>
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100.0%; Pred. No. 1.48+02;
cive 0; Mismatches 0; Indels
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25.0%; Score 5; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
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us-10-066-965a-1.oligo.rpr

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A;Genetic code: SGG4
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-ase
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                                                                         A;Molecule type: mRNA
A;Residues: 1-133 «KAL»
A;Cross-references: UNIPROT: P31628; GB:M63105; NID: G323291; PIDN: AAA42893.1; PID: G323392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nilternate names: cytochrome oxidase I
C; Species: mitochondrion Carabus violaceus
C; Species: mitochondrion Carabus violaceus
C; Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C; Accession: 857492
R; Howland, D.E.; Hewitt, G.M.
R; Howland, D.E.; Howland, G.M.
R; Howland, G.M.
R; Howland, G.M.
R; Howland, G.M.
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R;Howland, D.E.; Hewitt, G.M.
submitted to the EMBL Data Library, May 1995
A;Description: Phylogeny of the Coleoptera based on mitochondrial cytochrome oxidase I
A;Reference number: S57491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome-c oxidase (EC 1.9.3.1) chain I - Carabus violaceus mitochondrion (fragment)
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C;Species: mitochondrion Lucanus cervus
C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
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C,Superfamily: caprine arthritis-encephalitis virus rev-like protein
C,Keywords: splicing protein; transcription regulation
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No. 1.4e+02; Indels
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
A;Reference number: A40479; MUID:91306466; PMID:1649509
A;Accession: A40479
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100.0%; Pred. No. 1.4
:ive 0; Mismatches
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Best Local Similarity
Matches 5; Conserv
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A;Genome: mitochondrion
A;Genetic code: SGC4
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A,Molecule type: DNA
A,Residues: 1-133 <HOW>
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A; Residues: 1-133 <HOW>
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S57491
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A;Cross-references: UNIPROT:P73694; EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA1774
A;Nores-references: UNIPROT:P73694; EMBL:D4 EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s111698
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                                                                                                                                                                                                                                                                                            C;Species: Symechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S77183
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nalternate names: rev-like protein
C;Species: captrine arthritis-encephalitis virus, CAEV
C;Species: captrine arthritis-encephalitis virus, CAEV
C;Date: 30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: F45345
R;Saltarelli, M; Querat, G.; Konings, D.A.M.; Vigne, R.; Clements, J.E.
N;Italesy 179; 347-334, 1990
A;Title: Nucleotide sequence and transcriptional analysis of molecular clones of CAEV A;Reference number: A45345; MUD:91021037; PMID:2171210
A;Accession: F45345
A;Molecule type: mRNA
A;Residues: L133 scALDs
A;Accession: Airthorn 1913 scALDs
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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0
                                                                                                                                                                                                                                                          hypothetical protein sll1698 - Synechocystis sp. (strain PCC 6803)
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A,Accession: S77183
A,Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.0%; Score 5; DB 2; Length 126;
100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0; Indels
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C,Genetics:
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
                                  LWALG 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 LWALG 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
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C; Superfamily: c
C; Keywords: spli
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                                                                                                                                                                                RESULT 63
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C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: 180172
E;Accession: 180172
E;McAdam. S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5839-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544; PMID:8016085
A;Accession: 180172
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-137 <RES>
A;Cross-references: UNIPROT:Q95531; EMBL:U05583; NID:9454783; PIDN:AAA50186.1; PID:94547C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession. 180175
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544; PMID:8016085
A;Accession: 180175
A;Accession: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession. 180173
C;Accession. 180173
R;McAdam, S.N.; Boyson, J.B.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.B.; Watkins Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544; PMID:8016085
A;Accession: 180173
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Desiduan - Type - DNA
A;Desiduan - Type - Typ
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A,Residues: 1-137 <RES>
A,Cross-references: UNIPROT:Q95534; EMBL:U05586; NID:g454789; PIDN:AAA5018:
C,Superfamily: class I histocompatibility antigen; immunoglobulin homology
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ches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.5
Matches 5; Conservative 0; Mismatches
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Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180175
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D55511
D5MF 3'-region hypothetical protein - Pseudomonas sp. (strain KKS012)
C;Species: Pseudomonas sp.
C;Species: Pseudomonas sp.
C;Species: Pseudomonas sp.
C;Accession: D5551
SKiuchi, Y.; Yasukochi, Y.; Nagata, Y.; Pukuda, M.; Takagi, M.
J; Bacteriol. 176, 4269-4276, 1994
A;Title: Nucleotide sequence and functional analysis of the meta-cleavage pathway involv A;Reference number: A55511; MUID:94292455; PMID:8021212
A;Accession: D55511
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KIK>
A;Residues: 1-136 <KIK>
A;Cross-references: GB:D16407; NID:g303760; PIDN:BAA03894.1; PID:g425215
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; O'Gaora, P.; Cronin, P.; C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MulD:21534947; PMID:11677608
A;Reference number: AB0502; MulD:21534947; PMID:11677608
A;Residues: 1-133 cPAR>
A;Residues: 1-133 cPAR>
A;Residues: 1-133 cPAR>
A;Cross-references: GB:AL513382; PIDN:CAD08125.1; PID:g16505104; GSPDB:GN00176
C;Genetics:
A;Gene: yrfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein yrfA [imported] - Salmonella enterica subsp. enterica ser C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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F;90/Binding site: magnesium (His) (shared with chain II) #status predicted F;98/Binding site: heme a3 iron (His) (axial ligand) #status predicted
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                                                                                                                        Query Match 25.0%; Score 5; DB 2; Length 133; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: O'-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 138875
R;Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefand Immunogenetics 42, 19-27, 1995
A;Title: H.A.B alleles of the Gayapa of Ecuador: new B39 and B15 alleles.
A;Reference number: 138860; MUID:95317819; PMID:7797264
                                                                                                                                                                                                                                                                                                    R;McAdam, S.D.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: I59308; MUID:94286544; PMID:8016085
A;Accession: 180176
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-137 <RES
A;Cross-references: UNIPROT:095535; EMBL:U05587; NID:9454791; PIDN:AAA50190.1; PID:94547
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Species: Pan troglodytes (chimpanzee)
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C,Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Cross-references: UNIPROT:Q95533; EMBL:U05585; NID:g454787; PIDN:AAA50188.1; PID:g4547
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: 180176
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25.0%; Score 5; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Matches 5; Conservative 0; Mismatches 0; Indels
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                               1825181 segs, 575374646 residues
                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                      Post-processing: Listing first 100 summaries
                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                     BAD17451
BAD17502
Q6Z4J8
BAC83842
                                                                                                                                                                                                                                                                                                                                                                       Q8VWR7
Q840I0
Q73NA1
AAS11772
                                                                                20
                                                                                                  Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                      O7NUL1
Q9HNK5
Q88G85
Q6YXZ8
Q8G7W5
                                                                                                                                                                                                                                                                                                                                                     Q7YBD3
Q8HHU6
Q8SI37
                                                                                                                                                                                                                                                                                                                                                                                                                  Q8HAT7
Q8HAT8
Q8HAT9
Q8HAU0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8HAU1
Q8HAU2
Q8HBY9
Q8HI88
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Q7CXS4
                                                                                                                                                                                                                                                                    29I0H7
                                                                                                                                                                                                                                                                                                                                                                                                       28HATS
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                                                                                                                                                                                                                                                                                                                                               28HGD3
                                                                              1 QVWSLWALGWRWLRRYGWNM
                                                                                                                                                                                 UniProt_02:*
.: uniprot_sprot:*
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                                                                                                                                                   length: 0
length: 2000000000
                                                                US-10-066-965A-1
20
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                                          Run on:
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43 VWSLWALG 50
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PIR; AG2839; AG2839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=176299;
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01-MAR-2004
01-MAR-2004
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STRAIN=ATCC 15692 / PAO1;

STRAIN=20437337; pubmed=10984043;

SLOVET CK., PRAM X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nester E.W.; "The genome of the natural genetic engineer Agrobacterium tumefaciens
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MEDLINE-21608550; PubMed=11743193;
MEDLINE-21608550; PubMed=11743193;
MCDLINE-21608550; PubMed=10.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome, Hypothetical protein.
SEQUENCE 297 AA, 33197 MW, 0DF94B92126D72D5 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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100.0%; Pred. No. 0.67;
tive 0; Mismatches
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                                                                                                                               297 AA
                                                                                                                                                                                                               Created)
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                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                            (TrEMBLrel. 24,
                                                                                                                                                                                                           (TrEMBLrel. 16,
                                                                                                                                                                                                                                                      (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=PA2661;
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                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                  Hypothetical protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
                                                                                                                                                                                                                                         01-MAR-2001
01-JUN-2003
                                                                                                                                                                                                           01-MAR-2001
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Q8UDI2
                                      RESULT 1
20910H7
11D 0910H7
101-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                              Gaps
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro: IPR002293; AA/rel_permease1.
InterPro: IPR000055; HTHAArd.
InterPro: IPR004841; Permease_region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                       DB 2; Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 518;
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                                                                                                                                                                                   Pfam; PF00124; AA_permease; 1.
PROSTIE; PS00041; HTH ARAC FAMILY 1; UNKNOWN 1.
Complete proteome; Transmembrane; Transport.
SEQUENCE 504 AA; 54004 MW; 2028A16BB07D2461 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00324; AA_permease; 1.
PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                       Score 8; DB 2;
Pred. No. 1;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 AA
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100.0%; Pred. No. 1.1
cive 0; Mismatches
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EMBL, AE008130, AAK87890.1;
InterPro; IPR002293, AA/rel_permeasel.
InterPro; IPR000005; HTHARAC.
InterPro; IPR004841; Permease_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Cereon;
MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                 40.0%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=AGR_C_3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 26, TrEMBLrel. 26, TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                       Query Match 40.0
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
OrderedLocusNames=PP3840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         5 LWALGWR 11
                                                                                                                                                                                                                                                                                                                                                                                                                      28 LWALGWR 34
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 WLRRYG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 WLRRYG 74
                                 NCBI_TaxID=64091;
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01-JUN-2003
01-JUN-2003
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Matches
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                                                                                                                                             RA MEDDINE-LESSENGENCY (LURREGE 1470/182)

RA ANDORON R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,

Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,

Alves-Gomes J.A., Andrade B.M., Araripe J., de Araujo M.F.F.,

RA Astolfi-Filho S., Azevedo V., Baptista A.J. Bataus L.A.M.,

Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,

RA Carezynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,

RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fergundes N., Falcao C.L.,

RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

RA Gazzinelli R.T., Gomes E.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Gazzinelli R.T., Gomes E.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Gazzinelli R.T., Gomes E.C., Prelitas N.S.A., Furlan L.R.,

RA Machinelli P., Rains I.P., Fellas N.S.A., Furlan L.R.,

RA Gazzinelli R.T., Gomes E.C., Panna B.S., Jardim S.N., Laurino J.,

RA Gazzinelli R.T., Gomes E.C., Panna B.S., Jardim S.N., Laurino J.,

RA Gazzinelli R.C., Gomes E.C., Panna B.S., Jardim S.N., Laurino J.,

RA Machine R.M., Pintol L.S.A., Loureiro M.F., Lyra M.C.C.P.,

RA Mascimento F.F., Nicolas M.F., Cliveira J.G., Oliveira S.C.,

RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,

RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli B.,

Santos E.B., Santos F.R., Schneider M.P., Silva R., Simoes I.C.,

Silva A.M.R., da Silva A.L.C., Silva R., Simoes I.C.,

Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R.,

Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,

Vettore A., Wassem R., Zaha A., Sonza E.M., Souza E.M., Souza E.M.,

Proc. Natl. Acad. Soi. U.S.A. 100:11660-11665 (2003).

Probably responsible for the translocation of the substrate across

Proposition of the substrate across
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the membrane (By similarity).
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
--- SIMILARITY: Belongs to the binding-protein-dependent transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                            Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Chromobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=VNG2064H;
Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7; DB 2;
; Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 AA.
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GO, GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Transmembrane; Transport
Probable ABC trasporter, permease protein.
OrderedLocusNames=CV2686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                     STRAIN-ATCC 12472 / DSM 30191;
MEDLINE-22882880; PubMed=14500782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000515; BPD transp. Pfam; PF00528; BPD transp 1; 1. PROSITE; PS50928; ABC_TM1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                Chromobacterium violaceum.
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system permease famil
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                                                                                                     SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=536;
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01-MAR-2004
Vng2064h.
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MEDLINE=20504483; PubMed=11016950;
MEDLINE=20504483; PubMed=11016950;
MA Shukla H.D., Lasky S.P., Mahairas G.G., Berquist B., Pan M.,
Ng W.Y., Kennedy S.P., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.P., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Ung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,
T. Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
REMBL, ARGOS97; AAGZO215.1; -.
REMBL, REMOS97; AAGZO215.1; -.
ROMPLete proteome.
SCOMPLET BY REMOSE STI AA, 61059 MW; ED66FC0A7D35C176 CRC64;
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Welson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P. Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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SEQUENCE 74 AA; 8550 MW; 5F7FEBFB63468BD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%; Score 6; DB 2;
100.0%; Pred. No. 36;
:ive 0; Mismatches
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100.0%; Pred. No. 15;
iive 0; Mismatches
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BAD17502;
10-MAY-2004 (TERMELRE1. 27, Created)
10-MAY-2004 (TERMELRE1. 27, Last sequence update)
10-MAY-2004 (TERMELRE1. 27, Last annotation update)
10-MAY-2004 (TERMELRE1. 27, Last annotation update)
Hypothetical protein OSUNBb0056122.58.
OSUNBB0056122.58
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
                                                                                                                  Oryza sativa (japonica cultivar-group).
Mkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoldeae; Oryzea; Oryza; Oryza sativa.
                                                                                                                                                                                                                                     Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. Nipponbare;
Sasaki T., Matsumcto T., Katayose Y.;
Sasaki T., Matsumcto T., Katayose Y.;
Clone:OSJNBb0056122.";
Submitteed (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005644; EAD17502.1; -.
Bypothetical protein.
SEQUENCE 100 AA; 10960 MW; CC21D0B5AFBD0E4D CRC64;
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Last sequence update)
Last annotation update)
                              10-MAX-2004 (TrEMBLrel. 27, Created)
10-MAX-2004 (TrEMBLrel. 27, Last sequence update)
10-MAX-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBb0046012.18.
OSJNBB0046012.18.
                                                                                                                                                                                                                                                                                                                                                                                            30.0%; Score 6; DB 2;
100.0%; Pred. No. 46;
iive 0; Mismatches
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100 AA
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=39947;
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                                                                                                                                                                                                                           SEQUENCE
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Q6Z4J8;
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ID Q6
AC Q6
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MEDLINB=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Schell M.A., Xarmirantzou M., Snel B., Vilanova D., Berger B.,
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pridmore R.D., Arigoni F.;
"The genome sequence of Bifidobacterium longum reflects its adaptation
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                        Oryza sativa (japonica cúltivar-group).
Mukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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OrderedLocusNames=BL0120;
Bifidobacterium longum.
Bacteria, Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
                                                                05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBD0056122.58 (Hypothetical protein
OSJNBBD0046012.18)
Name-CSJNBD0056122.58; Synonyms=OSJNBD0046012.18;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 100; 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                             Sašaki T., Matsumoto T., Katayose Y.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005644; BAD17502.1; -.
EMBL; AP005643; BAD17451.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003425; Unk YGGT.
Pfam; PF02325; YGGT; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 100 AA; 11654 MW; 7B219E7C9B016BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 100 AA; 10960 MW; CC21D0B5AFBD0E4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL; AE014627; AAN21985-1; -.
GO; GO:0016020; C:membrane; IEA.
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100.0%; Pred. No. 46;
iive 0; Mismatches
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                     100 AA
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100.0%; Pred. No.
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                     PRT;
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                                                    (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 23,
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                     PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 WRWLRR 15
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05-JUL-2004
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                     Q6YXZ8
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Gaps

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Matches

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RESULT 8

Q8G7W5

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Gaps

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RESULT 9 BAD17451

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MEDLINE=22454480; PubMed=12565034;
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Matches 6; Conserv
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Neoptera; Paraneoptera; Phthiraptera; Amblycera; Menoponidae; Dennyus.
NCBI_TaxID=60508;
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                 Oryza sativa (japonica cultivar-group).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
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                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 101;
                                                                                                                                                          Length 101
                                                                                                                                                                               0; Indels
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                                                                                          Sasaki T., Matsumoto T., Katayose Y.;
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP005172; BAC83842.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone:OSJNBb0002201.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AP005172; BAC83842.1; -.
                                                                                                                                     101 AA; 10261 MW; 238F8F70BF4D8092 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AA; 10261 MW; 238F8F70BF4D8092 CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                              101 AA
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                                                                                                                                                        30.0%; Score 6; DB 2
100.0%; Pred. No. 47;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01 MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence
01-077-2003 (TrEMBLrel. 25, Last annotat.
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                     BAC83842;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last seque
02-MAR-2004 (TrEMBLrel. 27, Last annot
Hypochetical protein OSJNBb0002J01.11.
OSJNBB0002J01.11.
protein OSJNBb0002J01.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                               6; Conservative
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                                                                                                                                                                                                                                                                             PRELIMINARY;
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        Name=OSJNBb0002J01.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
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                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                    10 WRWLRR 15
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                                                                                                                                                                                                                       66 WRWLRR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                            NCBI_TaxID=39947;
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                                                                                                                                     SEQUENCE
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                                                                                                                                                          Query Match
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Matches
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Q8HGD3
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(Insecta: Phthiraptera).";
Mol. Phylogenet. Bvol. 26:231-242(2003).
-!- FNWCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C + 2 H(2)0.
--- PATHWAY: Respiratory chain; terminal step.
--- SUBCELLUIAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (8y similarity).
--- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; AF545694; AA011921.1; ---
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"Molecular systematics of Psocomorpha (Psocoptera).";
Syst. Entomol. 28:409-416(2003).
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Johnson K.P., Cruickshank R.H., Adams R.J., Smith V.S., Page R.D., Clayton D.H.;
                                                                                            "Dramatically elevated rate of mitochondrial substitution in lice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Psocoptera; Trogiomorpha; Lepidopsocidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copper; Electron transport; Heme; Limet measure, Transmembrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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GO; GO:0019866; C:inner membrane; IEA.
GO; GO:001671; C:integral to membrane; IEA.
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000883; COXI.
PFam; PF00115; COXI; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
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Transport.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Respiratory chain; terminal step.
-!- SUBMERLUULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity)
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
  = 4 ferricytochrome
                                     -1- PATHWAY: Respiratory chain; terminal step.
-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (8y similarity).
-1- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; AX275298; AAP97116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Phthiraptera; Amblycera; Menoponidae; Dennyus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                        Copper, Blectron transport, Heme, Inner membrane, Membrane,
Mitochondrion, Oxidoreductase, Respiratory chain, Transmembrane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:000746; C:mitcochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitcochondrion; IEA.
GO; GO:0005739; F:cytochrome-c oxidase activity; IEA.
                                                                                                                                   GO, GO:001966; C:inner membrane; IEA.
GO; GO:0016021; C:inner membrane; IEA.
GO; GO:0016729; C:integral to membrane; IEA.
GO; GO:0016739; C:inttochondrial electron transport chain; IEA.
GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:cytochrome-c ransport; IEA.
GO; GO:00166118; P:clectron transport; IEA.
InterPro; IFR000883; COXI.
Fransport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIANE=21655504; PubMed=11796033;
Johnson K.P., Whiting M.F.;
"Multiple genes and the monophyly of Ischnocera (Insecta:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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127 127
127 AA; 13609 MW; 6E961D920A3C9767 CRC64;
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Last annotation update)
  CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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01-MAR-2003 (TrEMBLrel. 23, Last sequenc
01-007-2003 (TrEMBLrel. 25, Last annotat
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6; 1
Pred. No.
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100.0%;
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SEQUENCE
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"Extraordinary sex ratios and the evolution of male neoteny in sibmating Ozopemon beetles.";

"Extraordinary sex ratios and the evolution of male neoteny in sibmating Ozopemon beetles.";

Biol. J. Linn. Soc. Lond. 75:353-360(2002).

-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mitochondrion, Oxidoreductase, Respiratory chain, Transmembrane,
                                                                                                                                                       Copper; Blectron transport; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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127 127
127 AA; 13691 MW; 4BA5B95D16A56F7F CRC64;
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GO; GO:0005746; C:mitochondrial electron transport ch
GO; GO:0005739; C:mitochondrial electron transport ch
GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
GO, GO:0016491; F:oxidoreductase activity, IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006810; P:transport; IEA.
PICAFPRO; IPRO0083; COXI.
Picam; PF00115; COXI; 1.
PRINTS; PR01165; CYCOXIDASEI.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity luv.v.
Best Local Similarity
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Pfam; PF00115; COX1; 1.
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Gaps

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SEQUENCE FROM N.A.

SIGNIBLE FROM N.A.

SEQUENCE STAIN=ATCC 35405 / DSM 14222;

X PubMed=15064399; DOI=10.1073/puas.0307639101;

A Schaddri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F., Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

A Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,

Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,

A Gebregeorgis E., Geer K., Tsgaye G., Malek J.A., Ayodeji B.,

Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,

A Vashisth P., Moneill T.Z., Xiang Q., Sodergren E., Baca E.,

Meinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;

"Comparison of the genome of the oral pathogen Treponema denticola
T with other spirochere genomes ":

Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

R EMBL; AE017250; AAS11772.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBL_TaxID=158;
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     Indels
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                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Score 6; DB 2 Similarity 100.0%; Pred. No. 71; 6; Conservative 0; Mismatches
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                             PRT;
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Pfam; PF01713; Smr; 1.
SMART; SM00463; SMR; 1.
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STRAIN=ATCC 35405 / DSM 14222;
PubMed=15064399;
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                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=TDE1254;
     6; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                           Treponema denticola.
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                                                                                                 124 WLRRYG 129
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Best Local Similarity
Matches 6; Conserv
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                                                    12 WLRRYG 17
                                                                                                                                                                                                                                                                                                                                                         Smr domain protein
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AAS11772
     Matches
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Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Amaryllidaceae,
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                          Length 134;
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Kim J.J., Lawrence J.E., Kluepfel D.A.;

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY163858; AAP30022.1; -.

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 AA; 15957 MW; E56ABB6F1F30879F CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
Transporter-like protein (Fragment)
Narcissus pseudonarcissus (Daffodil)
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                          DB 2;
                                                    59,
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100.0%; Pred. No. 62;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                      143 AA
                                    100.0%; Prec. ...
                          30.0%; Score 6;
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Query Match
Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                97 SLWALG 102
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                           4 SLWALG 9
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                              Q8VWR7;
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                                                                                                                                                                                                                                                                                                      Q8VWR7
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Q84010
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Gaps

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171 AA; 19210 MW; FB9848BF92FC0DEC CRC64;

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SEQUENCE
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                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inner membrane (By similarity).

-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.

EMBL; AB083742; BAC44946.1; -.

EMBL; AB083743; BAC44946.1; -.

EMBL; AB083743; BAC44947.1; -.

GO; GO:0019665; C:inner membrane; IEA.

GO; GO:00196746; C:inntegral to membrane; IEA.

GO; GO:0005746; C:initegral to membrane; IEA.

GO; GO:000129; C:initedral electron transport chain; IEA.

GO; GO:000129; F:cytochrome-c oxidase activity; IEA.

GO; GO:0006411; F:oxidoreductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                  Gaps
              Fraser C.M., Paulsen I.T.;
"Comparison of the genome of the oral pathogen Treponema denticola with other spirochete genomes";
Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

BMBL, AB017256, AAS11772.1;
TIGR: TDE1254;
TIGR: TDA39 MW; 9A29EB2307D04319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PROII65; CYCOXIDASBI.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanzaki N., Futai K.;
"Phylogenetic analysis of the phoretic association between
Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and
Psacothea hilaris (Coleoptera: Cerambycidae).";
Xiang Q., Sodergren E., Baca E., Weinstock G.M., Norris S.J.
                                                                                                                                                                         DB 2; Length 170;
                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit 1 (Fragment).
                                                                                                                                                           30.0%; Scor.
100.0%; Pred. No. /+/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=CO1;
Psacothea hilaris yonaguniana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000883; COX1.
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
171
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Best Local Similarity
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                                                                                                                                                                                                                                                                           ||||||
54 WLRRYG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=192788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                CHAT4;
                                                                                                                                                                                                                                                                                                                                                                                            OBHAT4
                                                                                                                                                                                                                  Matches
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-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and copper B (By similarity).

--- CATANTYIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)0.

--- PATHWAY: Respiratory chain; terminal step.
--- SUBGEBLULLAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
--- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AB083751; BAC44954.1; --
R EMBL, AB083751; BAC44954.1; --
R EMBL, AB083751; BAC44956.1; --
R EMBL, AB083752; BAC44957.1; --
R GO; GO:0019866; C:inner membrane; IEA.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0005746; C:integral to membrane; IEA.
R GO; GO:0005739; C:mitochondrial electron transport chain; IEA.
R GO; GO:00054129; F:cytochrome-c oxidase activity; IEA.
R GO; GO:0006119; F:cxidoreductase activity; IEA.
R GO; GO:0006119; F:cxidoreductase activity; IEA.
R GO; GO:0006110; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01165; CYCOXIDASEI.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                        0;
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Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanzaki N., Futai K., Phylogenetic association between "Phylogenetic analysis of the phoretic association between Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and Psacothea hilaris (Coleoptera: Cerambycidae).";
                    Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 171;
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                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Cytochrome oxidase subunit 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Score 6; DB 2;
100.0%; Pred. No. 72;
Live 0; Mismatches
                 DB 2;
30.0%; Scc...
100.0%; Pred. No. /r,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                171 AA
                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=CO1;
Psacothea hilaris miyakoana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000883; COX1.
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                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                       15 SLWALG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00115; COX
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                                                                                                                                4 SLWALG
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              Q8HAT7
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                                                                                                                                                                                                                                                                                                                                               FUNCTION: Cytochrome coxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and home A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
BMBL; AB083760; BAC44964.1; -.
BMBL; AB083761; BAC44965.1; -.
BMBL; AB083761; BAC44965.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Respiratory chain; terminal step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00115; COX1; 1.
PRINTS; PR01165; CYCOXIDASEI.
COpper; Electron transport; Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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EMBL; AB083762; BAC44966.1; -.
EMBL; AB083762; BAC44967.1; -.
EMBL; AB083762; BAC44967.1; -.
EQ; GO:0016921; C:intregral to membrane; IEA.
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:000419; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:cytochrome-c oxidase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                    Kanzaki N., Futai K., "Phylogenetic association between "Phylogenetic analysis of the phoretic association between Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and Psacothea hilaris (Coleoptera: Cerambycidae)."; Nematology 4:759-771(2002)
                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.0%; Score 6; DB 2; Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 AA; 19210 MW; FB9848BF92FC0DEC CRC64;
                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72;
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                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last annotate Cytochrome oxidase subunit 1 (Fragment) Name=CO1;
                                                                                                              Created)
                                                                                                        (TrEMBLrel. 23, C
(TrEMBLrel. 23, I
(TrEMBLrel. 27, I
                                                                                                                                                                       Psacothea hilaris maculata.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000883; COX1.
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                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
                       15 SLWALG 20
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                                                                                                                                                                                                                                               NCBI_TaxID=192793;
4 SLWALG 9
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                                                                                                             01-MAR-2003
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                                                                                    OBHAT6
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Matches
                                                           RESULT 23
                                                                        Q8HAT6
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SLWALG 20

15

RESULT 24

4 SLWALG 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and copper B (By similarity).
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
-!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inner membrane (By similarity).

-I. SIMILARITY: Belongs to the heme-copper respiratory oxidase family.

EMBL; AB083764; BAC44968.1; -.

EMBL; AB083765; BAC4469.1; -.

EMBL; AB083765; BAC44970.1; -.

GO; GO:0019866; C:inner membrane; IEA.

GO; GO:00198766; C:inner membrane; IEA.

GO; GO:0019746; C:mitochondrial electron transport chain; IEA.

GO; GO:0005739; C:mitochondrial electron transport chain; IEA.

GO; GO:0004199; F:cytochrome-c oxidase activity; IEA.

GO; GO:0016189; P:cytochrome-c oxidase activity; IEA.

GO; GO:0016191; P:coxidoreductase activity; IEA.

GO; GO:0006119; P:lectron transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copper; Electron transport; Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Chrysomeloidea, Cerambycidae, Lamiinae, Agniini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 171;
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                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit 1 (Fragment).
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171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 6; DB 2; Pred. No. 72; 0; Mismatches
PRT;
                                                                                                                                                                                                      Psacothea hilaris macronotata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.0%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR01165; CYCOXIDASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000883; COX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00115; COX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=192794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLWALG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SLWALG 9
                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                             Psacothea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8HAT8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSHATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8HAT8
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 SLWALG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=192795;
                                       NCBI_TaxID=192792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SLWALG 9
                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          -1- CATALYTIC AC
c + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fransport.
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=CO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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à
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                                                                                                                                                                                 Psacothea hilaris (Coleopters: Geramboidae).",
Nematology 4:759-771/2002).
-!-FUNCTION: Cytochrome c oxidase is the component of the respiratory of a formathe functional core of the enzyme complex. Co is the catalytic subunit of the enzyme complex. Co is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                  inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; AB083744; BAC44948.1; -.
EMBL; AB083745; BAC44949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                              c + 2 H(2)O.
-!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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GO, GO:0016021; C:inner membrane; IEA.
GO, GO:0005739; C:intcochondrial electron transport chain; IEA.
GO, GO:0005739; C:mitochondrial IEA.
GO; GO:0005739; C:mitochondrial IEA.
GO; GO:000419; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:cytochrome-c oxidase activity; IEA.
GO; GO:001619; P:electron transport; IEA.
GO; GO:0006118; P:transport; IEA.
FFGO:0006810; F:transport; IEA.
FFGO:0006810; C:mitochrome-complexity IEA.
FFGO:0006810; F:mitochrome-complexity IEA.
FFGO:0006810; F:mitochrome-complexity IEA.
FFGO:0006810; F:mitochrome-complexity IEA.
FFGO:0006810; COXI: 1.
                                                                                                                                          Kañzaki N., Futai K.;
"Phylogenetic analysis of the phoretic association between
Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01165; CYCOXIDASEI.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 171; . 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 171 171 171 171 19848BF92FCODEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8HAT9;
Q1-MRA-2003 (TrEMBLrel. 23, Created)
01-MR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 6; DB 2
100.0%; Pred. No. 72;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   AB083746; BAC44950.1; -. AB083747; BAC44951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB083746; BAC44950.1; --
EMBL; AB083747; BAC44951.1; --
BMBL; AB083748; BAC44952.1; --
EMBL; AB083749; BAC44952.1; --
               Psacothea hilaris ishigakiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Psacothea hilaris intermedia.
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Best Local Similarity
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                                                                                                 NCBI_TaxID=192789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SLWALG 9
                                                                                                                                SEQUENCE FROM N.A.
                              Mitochondrion.
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=COl;
                                                                                       Sacothea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
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Q8HAT9
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Psacothea hilaris (Coleoppera: Cerambycidae).";
Nematology 4:759-771(2002).
-!-FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Blectrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
-!-CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; AB083756; BAC44960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Respiratory chain; terminal step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB083759; BAC44961.1; -...

REML; AB083759; BAC44961.1; -...

ROJ GO:0019866; C:inner membrane; IEA.

ROJ GO:0016021; C:integral to membrane; IEA.

ROJ GO:0016021; C:intechondrial electron transport chain; IEA.

ROJ GO:0005746; C:mitochondrian; IEA.

ROJ GO:0006739; C:mitochondrian; IEA.

ROJ GO:0006129; F:cytochrome-c oxidase activity; IEA.

ROJ GO:0016421; F:cxtochrome-c oxidase activity; IEA.

ROJ GO:001641; F:cxtochrome-c oxidase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PROILÉS; CYCOXIDASBI.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                               Kanzaki N., Futai K.;
"Phylogenetic analysis of the phoretic association between
Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.0%; Score 6; DB 2; Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 AA; 19210 MW; FB9848BF92FC0DEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytochrome oxidase subunit 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Kanzaki N., Futai K.;
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4 SLWALG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Psacothea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=CO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8HAU2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8HAU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 29
    STATE 
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                                                                                     -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Blectrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B [By similarity).
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Psacothea hilaris (Coleoptera: Cerambycidae).";
Nemacology 4:759-771(2002).
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
chain that catalyzes the reduction of oxygen to water. Subunits 1-
                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family. EMBL; AB083770; BAC44974.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                         c + 2 H(2)O.
PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AB083771; BAC44975.1; -
REMBL, AB083772; BAC44975.1; -
REMBL, AB083772; BAC44976.1; -
REMBL, AB083773; BAC44976.1; -
REMBL, AB083773; BAC44976.1; -
REMBL, AB083773; BAC44976.1; -
REMBL, AB083773; Clintegral to membrane; IEA.
RGO; GO:0015021; C:integral to membrane; IEA.
RGO; GO:0005746; C:intcochondrial electron transport chain; IEA.
RGO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
RGO; GO:0016491; F:cxidoreductase activity; IEA.
RGO; GO:0016491; F:cxidoreductase activity; IEA.
RGO; GO:0006118; P:electron transport; IEA.
RGO; GO:0006810; P:transport; IEA.
RGO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000893; COX1.
Pfam; PR00115; COX1; 1.
PRINTS; PR01165; CYCOXIDASEI.
COPPET; Electron transport; Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                   Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and
Psacothea hilaris (Coleoptera: Cerambycidae).";
Nematology 4:759-771(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Chrysomeloidea, Cerambycidae, Lamiinae, Agniini,
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"Phylogenetic analysis of the phoretic association between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Score 6; DB 2; Length 171; 100.0%; Pred. No. 72;
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171 171
171 AA; 19210 MW; FB9848BF92FC0DEC CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Best Local Similarity
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NON TER
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SEQUENCE
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3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
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Nematology 4:759-771(2002).

-!-FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO i is the catalytic subunit of the enzyme. Blectrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!-CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                           -1- IMILARITY: Belongs to the heme-copper respiratory oxidase family. EMBL; AB083776; BAC44980.1; -. EMBL; AB083776; BAC44981.1; -. EMBL; AB083778; BAC44981.1; -. GO; GO:0019866; C:inner membrane; IEA. GO; GO:0019866; C:inner membrane; IEA. GO; GO:0016621; C:integral to membrane; IEA. GO; GO:00105746; C:mitochondrial electron transport chain; IEA. GO; GO:0004129; E:cytochrome-c oxidase activity; IEA. GO; GO:00166118; P:electron transport; IEA. GO; GO:00166118; P:electron transport; IEA. GO; GO:0006810; P:transport; IEA. GO; GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                c + 2 H(2)0.
-!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane (By similarity).
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Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Chrysomeloidea, Cerambycidae, Lamiinae, Agniini,
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"Phylogenetic analysis of the phoretic association between
Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and
Psacothea hilaris (Coleoptera: Cerambycidae).";
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Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit 1 (Fragment).
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100.0%; Pred. No. 72;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 AA
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PRINTS; PR01165; CYCOX
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Best Local Similarity
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Mitochondrion.
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; ABO83779; BAC44938.1; -.
GO; GO:0019866; C:inner membrane; IEA.
                                                      SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
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-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
PATHWAY: Respiratory chain; terminal step. SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                               Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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                                                                                                         L; AB083768; BAC44972.1; -..
GO:0019866; C:inner membrane; IEA.
GO:0015861; C:integral to membrane; IEA.
GO:005746; C:mitochondrial electron transport chain; IEA.
GO:0005739; C:mitochondrion; IEA.
GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO:0014129; F:oxidoreductase activity; IEA.
GO:0006118; P:electron transport; IEA.
GO:000618; P:electron transport; IEA.
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Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
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Pfam; PF00115; COXI; 1.
PRINTS; PR01165; CYCOXIDASEI.
COpper; Electron transport; Heme; Inner membrane; Membrane;
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                                     inner membrane (By similarity).
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                                                                                            AB083769; BAC44973.1; -.
                                                                         AB083767; BAC44971.1; -.
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Psacothea hilaris hilaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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Best Local Similarity
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FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in
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CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
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-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
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-!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1165; CYCOXIDASEI.
COpper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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GO; GO:001966; C:inner membrane; IEA.
GO; GO:0016746; C:mitcochondrial electron transport chain; IEA.
GO; GO:0005746; C:mitcochondrial lectron transport chain; IEA.
GO; GO:0005739; C:mitcochondrial lectron transport GO; GO:0006491; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:cytochrome-c activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000883; COXI;
PFam; PF00115; COXI; 1.
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Kanzaki N., Futai K.;

"Phylogenetic analysis of the phoretic association between bylogenetic analysis of the phoretic absociation between Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and Psacothea hilaris (Coleoptera: Cerambycidae).";

Nematology 4:759-771(2002).
GO:0016021; C:integral to membrane; IEA.
GO:0005739; C:mitochondrial electron transport chain; IEA.
GO:0005739; C:mitochondrion; IEA.
GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO:0016491; F:oxidoreductase activity; IEA.
GO:0016491; F:electron transport; IEA.
GO:0006810; P:transport; IEA.
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Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
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Last annotation update)
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100.0%; Pred. No. 72;
tive 0; Mismatches
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01-MAR-2003 (TrEMBLrel. 23, Last sequen
01-CCT-2003 (TrEMBLrel. 25, Last amnota
Cytochrome oxidase subunit 1 (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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                                                                                                                                                                                                                                                                                                       Pfam; PF00115; COX1; 1
PRINTS; PR01165; CYCOX
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Best Local Similarity
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Pred. No. 72; ; Mismatches

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6; Conservative
 Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
                                                                                                                                                                                           Gaps
                 Copper; Electron transport, Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01165; CYCOXIDASEI.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Chrysomeloidea, Cerambycidae, Lamiinae, Agniini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanzaki N., Futai K.;
"Phylogenetic analysis of the phoretic association between
Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and
Baccathea hilaris (Coleoptera: Cerambycidae).";
Nematology 4:759-771(2002).
                                                                                                                                                     DB 2; Length 171;
                                                                                                                                                                                           Indels
                                                                                         171 171
171 AA; 19210 MW; FB9848BF92FC0DEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 AA; 19240 MW; FB9848A5385D1CEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               ol-MAR-2003 (TrEWBLrel. 23, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Cytochrome oxidase subunit 1 (Fragment).
                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                 171 AA.
                                                                                                                                                             100.0%; Pred ...
                                                                                                                                                   30.0%; Score 6; 1
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Psacothea hilaris intermedia.
PRINTS; PR01165; CYCOXIDASEI
                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                   15 SLWALG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=192792;
                                                                                                                                                                                                                             4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion
                                                     Transport.
                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Psacothea.
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NON TER
SEQUENCE
                                                                                                                                                     Query Match
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Q8H189;
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                           RESULT 32
                                                                                                                                                                                                                                                                                                                                             Q8H189
DR
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C + 2 H(2) C.

C - 1- PATHWAY: Respiratory chain; terminal step.

C - 1- SUBLELOLAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).

C - 1- SIMILARITY: Belongs to the heme-copper respiratory oxidase family. BEBL; AB08175: BAC44559: 1.

R GO; GO:0019866; C:inner membrane; IEA.

R GO; GO:001866; C:inner membrane; IEA.

R GO; GO:0018739; C:integral to membrane; IEA.

R GO; GO:0018739; C:integral to membrane; IEA.

R GO; GO:0018739; C:integral to membrane; IEA.

R GO; GO:0018739; C:intechondrial electron transport chain; IEA.

R GO; GO:0018419; F:cytochondrion; IEA.

R GO; GO:0018419; F:cytochorder exidase activity; IEA.

R GO; GO:0018610; P:cransport; IEA.

R GO; GO:0018610; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I-FUNCTION: Cytochrome coxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and copper B (By similarity).

CATALYIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PROII65; CYCOXIDASBI.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Kanzaki N., Futai K.;
"Phylogenetic analysis of the phoretic association between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.0%; Score 6; DB 2; Length 171; 100.0%; Pred. No. 72; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 AA; 19186 MW; B7389CEB97B91A51 CRC64;
                                                                                                                                                                                                                              01.MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome oxidase subunit 1 (Fragment).
                                                                                                                                                                    171 AA.
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                            Psacothea hilaris intermedia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.0
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00115; COX1; 1
15 SLWALG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=192792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 SLWALG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYT
                                                                                                                                                                                                                                                                                                                                                                    Name=CO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Psacothea
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NON TER
SEQUENCE
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RESULT 34

30.0%; Score 6; DB 2; Length 171;

Query Match

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Paracthea hilaris (Coleoptera: premarcula: principality and Psacothea hilaris (Coleoptera: Cerambycidae).";
Nematology 4:759-771(2002).
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3
                                                                                                                                                                                                                                                                                                                                                                                                                                        per B (By similarity).   
IC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; AB083740; BAC44944.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c + 2 H(2)0.
-!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
              Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera; Endopterygota; Coleoptera, Polyphaga, Cucujiformia;
Phytophaga, Chrysomeloidea; Cerambycidae; Lamiinae; Monochamini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016021; C:inner membrane; IEA.
GO; GO:0016021; C:inner membrane; IEA.
GO; GO:0005746; C:introchondrial electron transport chain; IEA.
GO; GO:0005739; C:introchondrion; IEA.
GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO; GO:0006118; P:oxidoreductase activity; IEA.
GO; GO:0006118; P:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006119; P:transport; IEA.
                                                                                                                                                                                                                         Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01165; CYCOXIDASEI.
Copper; Electron transport; Heme; Inner membrane; Membrane;
                                                                                                                                                         SEQUENCE FROM N.A.
Kanzaki N., Futai K.;
"Phylogenetic analysis of the phoretic association between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 AA; 19196 MW; 269D5136AE243DFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion; Oxidoreductase; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%; Score v, 100.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000883; COX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanseniella sp. EW-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00115; COX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=134582;
                                                                                                             NCBI_TaxID=192382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           and copper B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171
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Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARTY IN CALCIDION COXIDAGE is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-
3 form the functional core of the enzyme complex. Co I is the
catalytic subunit of the enzyme. Blectrons originating in
cytochrome c are transferred via the copper A center of subunit 2
and home A of subunit 1 to the bimetallic center formed by heme A3
and copper B (By similarity).
CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
Inner membrane (By similarity).
SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Membrane;
Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0019866; Cinner membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005739; C:integral to membrane; IEA.
GO; GO:0005739; C:inttochondrion; IEA.
GO; GO:0004129; F:oxtochrome-c oxidase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000883; COX1.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Agniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bursaphelenchus conicaudatus (Nematoda: Aphelenchoididae) and
Psacothea hilaris (Coleoptera: Cerambycidae).";
Nematology 4:759-771(2002).
                                                                                                                                                                                                                                                                                                                                                                                               Kanzaki N., Futai K.;
"Phylogenetic analysis of the phoretic association between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 AA; 19229 MW; 1E8C19FFC6FAA72A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome oxidase subunit 1 (Fragment).
                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Cytochrome oxidase subunit 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01165; CYCOXIDASEI.
Copper; Electron transport; Heme; Inner membrane;
Mitochondrion; Oxidoreductase; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 AA
                        171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.0%; Score 6; I
100.0%; Pred. No.
                                                                    Created)
                                                                                                                                                                                       Psacothea hilaris teneburosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=COl;
Monochamus alternatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00115; COX1;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=192791;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c + 2 H(2)0.
PATHWAY: Resi
                                                                                                                                                                                                             Mitochondrion.
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01-MAR-2003 (
01-MAR-2003 (
                                                                    01-MAR-2003
01-MAR-2003
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NON TER
SEQUENCE
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Thampapillai G.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Myriapoda; Symphyla; Scutigerellidae;
                                                                                             Last sequence update)
   184 AA.
                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequen
01-MAR-2004 (TrEMBLrel. 26, Last annota
Cytochrome oxidase subunit I (Fragment)
PRT;
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0;

Gaps

0;

0; Indels

DB 2; Length 171;

Transmembrane;

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inner membrane (By similarity).
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                                                                                                                                                                                                                                                                 EMBL; AE003945; AAF83909.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyperobius carinatus.
                                                                                                                                                                                                                                                                                     PIR; F82725; F82725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SLWALG 9
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chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
                                                                                                      and copper B (By similarity). CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                     PATHWAY: Respiratory chain, terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
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Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                        G0:0019866; Cinner membrane; IEA.
G0:0015021; C:inner membrane; IEA.
G0:0005739; C:mitochondrial electron transport chain; IEA.
G0:0005739; C:mitochondrian; IEA.
G0:0004129; F:cytochrome-c oxidase activity; IEA.
G0:0006118; P:electron transport; IEA.
G0:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000883; COXI.
Pfam; PF00115; COXI; 1.
PRINTS; PR01165; CYCOXIDASEI.
COpper; Electron transport; Heme; Inner membrane; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.0%; Score 6; DB 2; Length 184; 100.0%; Pred. No. 76; o; Indels ive 0; Mismatches 0; Indels
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Last annotation update)
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                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to t
EMBL; AF218271; AAK94875.1;
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                                                                                                                                                   + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!- CATALYIIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)0.

-!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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MEDLINE=21651553; PubMed=11794778;
Trewick S.A., Wallis G.P.;
"Bridging the 'beech-gap': New Zealand invertebrate phylogeography
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,

de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,

de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,

da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,

de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

"The genome sequence of the plant pathogen Xylella fastidiosa.";

Nature 406:151-159(2000).
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Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Curculionidae; Molytinae; Molytini; Lyperobius.
NCBI_TaxID=169099;
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GO:0015021; C:inner membrane; IEA.
GO:0005746; C:intechondrial electron transport chain; IEA.
GO:0006739; C:mitochondrion; IEA.
GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO:0016491; F:oxidoreductase activity; IEA.
GO:0016491; P:electron transport; IEA.
GO:0006810; P:transport; IEA.
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Evolution 55:2170-2180(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 191;
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Complete proteome; Hypothetical protein.
SEQUENCE 191 AA; 20144 MW, 4CD570C466BCFD11 CRC64;
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01-OCT-2002 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.0%; Score 6; DB 2;
100.0%; Pred. No. 79;
ive 0; Mismatches
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Interpro; IPR000326; Pesterase_PA_PTP.
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Nature 406:959-964(2000)
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Matches 6; Conserv
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SEQUENCE FROM N.A.
STRAIN=IMRU 3570;
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STRAIN=IMRU 3570;
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Matches
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Q9HYC6
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                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S., Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P., Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.; "Unique features revealed by the genome sequence of Acinetobacter Sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
InterPro; IPR000883; COX1.

Pfam; PF00115; COX1; 1.

PRINTS; PR01165; CYCOXIDASEI.

Copper; Blectron transport; Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
OrderedLocusNames=ACIAD3221;
Acinetobacter &p. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                 DB 2; Length 213; . 86;
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SEQUENCE 246 AA; 27971 MW; 99A44BC1DD082989 CRC64;
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213 213
213 AA, 23647 MW, B86440BEA5FD6AC8 CRC64;
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Last annotation update)
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 97;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 AA
                                                                                                                                                                                                 30.0%; Score 6; DB 2
100.0%; Pred. No. 86;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, CRS43861; CAG69905.1; -
InterPro, IPR006220; Anth synthii.
InterPro, IPR000991; GATase_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00117; GATase; 1.
PRINTS; PR00097; ANTSNTHASEII.
PRINTS; PR00096; GATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                             Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 RWLRRY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                     89 SLWALG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=62977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RWLRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thioesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=canT;
                                                                                                         Transport.
                                                                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        QGF7R0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9EWC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9EWC2
                                                                                                                                                                                                                                                                                                                                                                                                                      Q6F7R0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 40
QOBENC
LD QOBENC
AC QOBENC
DT 01-MA
DT
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                                                                                                                                                                                                                          Campelo A.B.;
Thesis (2000), Department of Microbiologia, Universidad de Leon, Leon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
MEDLINE=21642576; PubMed=11782498; Campelo A., Gil JA.; Campelo A.B.; "Gil JA.; "The candicidin gene cluster from Streptomyces griseus IMRU 3570."; Microbiology 148:51-59(2002).
                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA
GO; GO:0009058; P:biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.0%; Score 6; DB 2; Length 266; Similarity 100.0%; Pred. No. 1e+02; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%; Score 6; DB 2; Length 256;
100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR003006; Ig_MHC.
PROSTIRS, PS00290; IG_MHC; UNKNOWN 1.
Complete proteome; Hypothetical protein.
SEQUENCE 266 AA; 28619 MW; EB241FC27F0660F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00975; Thioesterase; 1.
SEQUENCE 256 AA; 28080 MW; F65C9F94E11857E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000379; Ser estrs.
InterPro; IPR001031; Thioesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004769; AAG06871.1; -. PIR; D83210; D83210.
                                                                                                                                                                                                                                                                                                                        EMBL; AJ300302; CAC22116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
OrderedLocusNames=PA3483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen."
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Gaps

Q6VZ13

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Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Shakhova V.V., Belova G.I., Aravind L., Matale D.A., Koonin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malyk A.G., Koonin E.V., Kozyavkin S.A., "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";

"A seq. Sci.U.S.A. 99:4644-4649(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Organizational and mutational analysis of a complete FR-
008/candicidin gene cluster encoding a structurally related polyene
                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 26, Last sentotation update)
Uncharacterized protein specific for M.kandleri, MK-45 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces sp. FR-008.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
PubMed=14652074;
Probed=14652074;
Deng Z.;
                                                                                                                            DB 2; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.0%; Score 6; DB 2; Length 277; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                           270 270
270 AA; 30323 MW; 7A57C40E6ED5FDD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 AA; 30678 MW; 872BBDA9BB9E5F3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JÜL-2004 (TrEMBLrel. 27, Created)
05-JÜL-2004 (TrEMBLrel. 27, Last sequence update)
05-JÜL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                         Query Match 30.0%; Score 6; DB 2; Len Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=206662;
                                                                                                                                                                                                                                                                                                                                                                  277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 AA
                                                                                                                                                                                                                                                                                                                                                                  PRT;
EMBL; AY318914; AAR17105.1; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=MK1353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanopyrus kandleri
                                                                                                                                                                                                                                                        98 SLWALG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 WRWLRR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 WRWLRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 277 AA;
                                                                                                                                                                                                              4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanopyrus.
NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=fscTE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complex.";
                                          NON TER
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                        Q8TVNS;
                                                                                                                                                                                                                                                                                                                                                                Q8TVN5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 45
Q6W5Q5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                      RESULT 44
                                                                                                                                                                                                                                                                                                                                              Q8TVN5
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-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Co I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                  Klass K.-D., Picker M.D., Damgaard J., van Noort S., Tojo K.;
"The Taxonomy, Genitalic Morphology, and Phylogenetic Relationships of
South African Mantophasmatodea (Insecta).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Klass K.-D., Picker M.D., Damgaard J., van Noort S., Tojo K.;
"The Taxonomy, Genitalic Morphology, and Phylogenetic Relationships of
South African Mantophasmatodea (Insecta).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c + 2 H(2)O.
-!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01165; CYCOXIDASEI.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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Mantodea sp. JD-2003.
Mitochondrion.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Mantodea.
NCBI_TaxID=253121;
                                                                                                                                                                                   Mitochondrion.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Mantodea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.0%; Score 6; DB 2; Length 270; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
270 270
270 AA, 30323 MW, 7A57C40E6ED5FDD9 CRC64;
                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-WAR-2004 (TrEMBLrel. 27, Created)
C2-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                   270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY318914; AAR17105.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
InterPro; IPR000883; COX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Entomol. Abh. 61:3-67(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00115; COX1; 1
                                                                                                                                                                    Mantodea sp. JD-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 SLWALG 103
                                                                                                                                                                                                                                                   NCBI_TaxID=253121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLWALG 9
                 Q6VZ13;
Q6VZ13;
05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport.
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR17105;
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RESULT 43

g

0;

Gaps

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RESULT 46

g

à

AAQ82559

IID AAQ8

AAQ AAQA

AAQ AAQA

DJT 02-M

DJT 02-M

DJT 02-M

CO STIF

CO ST

Matches

RL DR DR DR SQ SQ

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Probably responsible for the translocation of the substrate across the membrane (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SUBCELLULAR Selongs to the binding-protein-dependent transport system permease family.
--- SIMILARITY: Belongs to the binding-protein-dependent transport system permease family.
--- GO; GO: 0016020; C: membrane; IEA.
--- GO; GO: 0008215; F: transporter activity; IEA.
--- GO; GO: 0008215; F: transporter activity; IEA.
--- InterPro; IPR000515; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                 -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947; Rocag G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P., Alloyren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.0%; Score 6; DB 2; Length 288; 100.0%; Pred. No. 1.1e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        Length 288;
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABC transporter for sugars, membrane component precursor.
                                                EMBL; BX569622, CAE07798.13.

EMBL; BX569622, CAE07798.13.

GO; GO:0005215; Fitznasporter activity; IEA.

GO; GO:0005215; Fitznasporter activity; IEA.

GO; GO:0005215; BPD_transp.

InterPro; IPR000515; BPD_transp.

Ffam; PF00528; BPD_transp.

PROBITE; PS50928; ABC_TMI; 1.

PROBITE; PS50928; ABC_TMI; 1.

PROBITE; PS50928; ABC_TMI; 1.

FROMILE profeeme; Signal; Transmembrane; Transport.

SIGNAL
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506FA8DF2D2E4825 CRC64;
                                                                                                                                                                                                                                                                          Potential.
: 0EF08A3C854BD843 CRC64;
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PROSITE; PS50928; ABC_TM1; 1.
Complete proteome; Signal; Transmembrane; Transport.
SIGNAL 288 288 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        DB 2; Ler
. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                        30.0%; Score 6; I
100.0%; Pred. No.
tive 0; Mismatch
membrane (By similarity).
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Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                288 AA; 31458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 AA; 32176 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      niche differentiation.";
Nature 424:1042-1047(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=PMT0693;
                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
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MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
Chain P., Lamerdin J.E., Regala W., Allen B.E., McCarren J.,
Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
"The 424:1037-1042(2003)

Nature 424:1037-1042(2003)

-! FUNCTION: Part of a binding-protein-dependent transport system.

Probably responsible for the translocation of the substrate across
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ABC transporter for possibly for trehalose/maltose, membrane component
                                                                                                                                                                                            Gaps
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008/Candicidin Gene Cluster Encoding a Structurally Related Polyene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
PubMed=14552074;
Chen S., Huang X., Zhou X., Bai L., He J., Jeong K.J., Lee S.Y.,
Deng Z.;
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                                                                                                                                              30.0%; Score 6; DB 2; Length 285; 100.0%; Pred. No. 1.1e+02; cive 0; Mismatches 0; Indels
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Chem. Biol. 10:1065-1076(2003).
EMBL; AY310323; AAQ82559.1; -.
SEQUENCE 285 AA; 31691 MW; FD3CA8EB2ABA7A92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor.
OrderedLocusNames=SYNW1283;
Synactorios Sp. (strain WH8102).
Bacteria: Cyanobacteria; Chrococcales; Synechococcus.
NCBI_TaxID=84588;
                                                                                    Pfam; PF00975; Thioesterase; 1.
SEQUENCE 285 AA; 31691 MW; FD3CABEB2ABA7A92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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Chem. Biol. 10:1065-1076(2003).
EMBL, AX100323, AA602559.1; -.
InterPro; IPR0010379; Ser estrs.
InterPro; IPR001031; Thioesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                    Similarity 100.
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces sp. FR-008.
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Best Local Similarity
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Best Local S
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Matches

RESULT 47

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Cytochrome oxidase subunit I (Fragment).
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Pfam; PF00115; COXI; 1.
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                                                                      NCBI_TaxID=124017;
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                                                                                          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                    Ozopemon brownei.
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NON_TER
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                                                                                                                                                                                                Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, ABCH7232, AAS03864.1; -
Complete proteome, Hypothetical protein.
SEQUENCE 295 AA; 33178 MW; 6AB11288695B3D04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li L., Barnantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017232, AAS03864.1; -.
Hypothetical protein.
SEQUENCE 295 AA; 33178 MW; 6AB11288695B3D04 CRC64;
                                                                                                                  Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae, Mycobacteriaceae, Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium,
                                                                                                                                                                                                                                                           30.0%; Score 6; DB 2; Length 295; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
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Last sequence update)
Last annotation update)
                                                                  05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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                                                  295 AA
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                                                                                                                                                  Mycobacterium avium complex (MAC)
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Q8SI38;
01-JUN-2002 (TEMBLEEL 21,
01-JUN-2002 (TEMBLEEL 21,
01-MAR-2004 (TEMBLEEL 26,
                                                                                                           OrderedLocusNames=MAP1547c;
                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100..
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                                                 PRELIMINARY;
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Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                        253 LGWRWL 258
112 ALGWRW 117
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                                                                                                                                                                                                                                                                                                    8 LGWRWL 13
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                                                                                                                                                            NCBI_TaxID=1770;
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AAS03864;
                                               Q73ZQ4
Q73ZQ4;
                             RESULT 49
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Extraordinary sex ratios and the evolution of male neoteny in sibmatraordinary sex ratios and the evolution of male neoteny in sibmatrial Ozopemon beetles.";

Biol. J. Linn. Soc. Lond. 75:353-360(2002).

-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!- GATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2) = C + 2 H(2) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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PROSITE: PS0077; COX1; 1.
CORDER: Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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0
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Phytophaga; Scolytidae; Ozopemon.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005746; C:integral to membrane; IEA.
GO; GO:0005739; C:introchondrion; IEA.
GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO; GO:0004189; F:cytochrome-c oxidase activity; IEA.
GO; GO:0006118; P:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006119; P:transport; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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330 AA;
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Matches 6; Conserv
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Q8SI28;
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                                                                             -!- FUNCTION: Cytochrome coxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Co I is the catalytic subunit of the enzyme. Bleckrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mating Ozopemon beetles.";
Biol. J. Linn. Soc. Lond. 75:353-360(2002).

-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-chain the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons oxiginating in
                                                                                                                                                                                         c + 2 H(2)0.
PATHWAY: Respiratory chain, terminal step.
SUBCELLUIAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
       Farrell B.D., Sequeira A.S., O'Meara B.C., Normark B.B., Chung J.H., Jordal B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jordal B.H., Beaver R.A., Normark B.B., Farrell B.D.; "Extraordinary sex ratios and the evolution of male neoteny in sib-
                                        "The evolution of agriculture in beetles (Curculionidae: Scolytinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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                                                                                                                                                                                                                                                                     GO; GO:0019866; C:inner membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0004129; C:witochondrian; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; P:ioxidoreductase activity; IEA.
GO; GO:0006810; P:electron transport; IEA.
InterPro; IPR000883; COXI.
PFEM; PF00115; COXI: 1.
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PROSITE; PS00077; COX1; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
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327 AA; 35766 MW; C81C79B2C01B47A9 CRC64;
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequenc
01-MAR-2004 (TrEMBLrel. 26, Last annotat.
Cytochrome oxidase subunit I (Fragment).
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 MEDLINE=21596578; PubMed=11761062;
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                                                    and Platypodinae).";
Evolution 55:2011-2027(2001).
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Best Local Similarity
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NON TER
SEQUENCE
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c. + 2 H(2)0.

d. + 2
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mating Ozopemon Deetles.";

Biol. 7. Linn. 80c. Lond. 75:353-360(2002).

-!-FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxegen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Blectrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!-CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
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-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; AF438519; AAM08283.1; -.
cytocorrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
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Jordal B.H., Beaver R.A., Normark B.B., Farrell B.D.,
"Extraordinary sex ratios and the evolution of male neoteny in sib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copper; Blectron transport; Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Scolytidae, Ambrosiodmus.
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Last annotation update)
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100.0%; Pred. No. 1.2
tive 0; Mismatches
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01-JUN-2002 (TrEMBLrel. 21, Last seqn
01-MAR-2004 (TrEMBLrel. 26, Last ann
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PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; 1.
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Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
         PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
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SEQUENCE
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Matches
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"Extraordinary sex ratios and the evolution of male neoteny in sib-
mating Ozopenon beetles.",

Biol. J. Linn. Soc. Lond. 75:353-360(2002).

-I-FUNCTION: Cytochrome c oxidase is the component of the respiratory
chain that catalyzes the reduction of oxygen to water. Subunits 1-
3 form the functional core of the enzyme complex. CO I is the
catalytic subunit of the enzyme. Blectrons originating in
cytochrome c are transferred via the copper A center of subunit 2
and heme A of subunit 1 to the bimetallic center formed by heme A3
and copper B (By similarity).

-I-CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
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R GO; GO:0019866; C:inner membrane; IEA.

R GO; GO:0016221; C:integral to membrane; IEA.

R GO; GO:0016221; C:integral to membrane; IEA.

R GO; GO:0016742; C:mitcochondrical electron transport chain; IEA.

R GO; GO:00129; F:cytochrome-c oxidase activity; IEA.

R GO; GO:001841; F:oxidoreductase activity; IEA.

R GO; GO:001841; F:oxidoreductase activity; IEA.

R GO; GO:001819; P:transport; IEA.

R GO; GO:001810; P:transport; IEA.

R Dfam; PR00185; CXCXI.

R Pfam; PR00185; CXCXI.

R PROSITE; PR00165; CXCXIDASEI.

R ROSITE; PS00077; COXI; I.

M COPPET; Electron transport; Heme; Inner membrane; Membrane;

M Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Scolytidae; Dryocoetes.
NCBI_TaxID=124009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%; Score 6; DB 2; Length 330; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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330 330
330 AA; 36037 MW; 71F436572CC8F42A CRC64;
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GO; GO:0016021; C:integral t
GO; GO:0005746; C:mitochondar
GO; GO:0005739; C:mitochondar
GO; GO:0004129; F:cytochrome
GO; GO:0016491; F:cytochrome
GO; GO:0016119; P:clectron t
GO; GO:0006119; P:clectron t
GO; GO:0006119; P:clectron t
Fem; PF00115; COX1; 1.
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Best Local Similarity 100.
Matches 6; Conservative
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NON TER
SEQUENCE
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Q8SI30;
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Biol. J. Linn. Soc. Lond. 75:353-360(2002).

Biol. V. Linn. Soc. Lond. Oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Blectrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jordal B.H., Beaver R.A., Normark B.B., Farrell B.D., "Extraordinary sex ratios and the evolution of male neoteny in sib-

    c + 2 H(2)O.
    -!- PATHWAY: Respiratory chain; terminal step.
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

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PROSTES; PSOONT; COX1; 1.
COPPER: Electron transport; Heme; Inner membrane; Membrane; Mitcchondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Scolytidae; Ozopemon.
NCBI_TaxID=124017;
                                                                                                                     / Match 30.0%; Score 6; DB 2; Length 330; Local Similarity 100.0%; Pred. No. 1.2e+02; les 6; Conservative 0; Mismatches 0; Indels
1 1
330 330
330 AA, 35836 MW, F72DB3B46742FEGE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 330
330 AA; 36024 MW; 5AA90D0F707E4956 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000883; COX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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30.0%; Score 6; DB 2; Length 330;

330 AA.

PRT;

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PRELIMINARY;
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                                                                                                                                                                                                             Ozopemon uniseriatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLWALG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLWALG 9
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                                                                                                                                                                                                                                  Mitochondrion.
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NON TER
NON TER
                                                                                                                                                                                    Name=CO1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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   8
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                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mating Ozopemon beetles.")
Biol. J. Linn. Soc. Lond. 75:353-360(2002).
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL, AF438513; AAM08277.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jordal B.H., Beaver R.A., Normark B.B., Farrell B.D.; "Extraordinary sex ratios and the evolution of male neoteny in sib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c + 2 H(2)0.
PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1165; CYCOXIDASBI.
PROSITE; PS00077; COX1; 1.
COpper; Electron transport; Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016745; C:intecproductial bectron transport chain; IEA.
GO; GO:0005739; C:mitochondrial bectron transport chain; IEA.
GO; GO:0004439; F:cytochrome-c oxidase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:001818; P:electron transport; IEA.
GO; GO:00068118; P:electron transport; IEA.
FILEPPRO: IPRO: GO:000811; C:XII.
FEAP.

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Pred. No. 1.2e+02;
                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36077 MW; 52B22651C6CE73AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Cytochrome oxidase subunit I (Fragment).
100.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.0%; Scor.
100.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                   330 AA
                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
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                              6; Conservative
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coccotrypes graniceps.
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330
330 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                        SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                               Q8SI34
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QBSI41
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                              Matches
                                                                                                                                                                                                                                        RESULT 57
                                                                                                                                                                                                                                                                       Q8SI34
                                                                                                                                                                                                                                                                                                   A SOLUTION TO THE PROPERTY OF 
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C + 2 H(2) C.

1 PATHWAY: Respiratory chain; terminal step.

1 - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).

1 - SIMILARITY: Belongs to the heme-copper respiratory oxidase family. R EMBL; AF438506; AAM08270.1; - C.

2 - SIMILARITY: Belongs to the heme-copper respiratory oxidase family. R GO; GO:0019866; C:inner membrane; IEA.

3 - GO; GO:001621; C:integral to membrane; IEA.

4 - GO; GO:001621; C:integral to membrane; IEA.

5 - GO:001621; C:integral to membrane; IEA.

6 - GO:001621; C:integral to membrane; IEA.

7 - GO:00164129; F:cytochrond-c oxidase activity; IEA.

8 - GO; GO:0016491; F:oxidoreductase activity; IEA.

8 - GO; GO:0016491; F:oxidoreductase activity; IEA.

9 - GO:001610; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Extraordinary sex ratios and the evolution of male neoteny in sibmating Ozopeann beetles.";
Biol. J. Linn. Soc. Lond. 75:353-360(2002).

"EVALVACION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

--- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PROILÉS; CYCOXIDASEI.
PROSTES; PSOONT; COX1; 1.
CORDER; Blectron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                    Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Scolytidae; Ozopemon.
NCBI TaxID=190778;
                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.0%; Score 6; DB 2; Length 330; 100.0%; Pred. No. 1.2e+02;
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Last annotation update)
                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                       Cytochrome oxidase subunit I (Fragment)
08S141,
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000883; COXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
OrderedLocusNames=PA2154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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2911M1
AC Q911W
AC Q911W
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
CGN Order
OC Bacte
OC Pseud
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OX RRP RRP RRA RRA RRA RRI RRI RRI DR KW KW KW KW KW

Пр

δ

0;

Gaps

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Cerambycidae, Laminae, Acanthocinini) on assessments of host, seasonal, and stratum specificity.";
Biol. J. Linn. Soc. Lond. 76:195-209(2002).
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Rlectrons oxiginating in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Acanthocinini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUDUENCE FAULT.

PubMed=15075281.

Bok J.W., Keller N.P.;

Bok J.W., Keller N.P.;

"LaeA, a regulator of secondary metabolism in Aspergillus spp.";

"LaeA, a regulator of S27-535(2004).

EMBL; AV42273; AAR01218.1;

InterPro; IPR000051; SAM bind.

InterPro; 349 AA; 40076 MW; 0462C78DlA7E82A0 CRC64;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The impact of redefined species limits in Palame (Coleoptera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Score 6; DB 2; Length 349; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                 30.0%; Score 6; DB 2; Length 337; 100.0%; Pred. No. 1.3e+02; ative 0; Mismatches 0; Indels
                                        1 1
337 337
337 AA, 36768 MW, FD20B47F8BAFF966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus fumigatus (Sartorya fumigata)
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                         Query Match
Query Match
Best Local Similarity 100.000
...haq 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                         247 SLWALG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 SLWALG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=185376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                              4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palame mimetica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
                     Transport.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berkov A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=COI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DBSEB6;
                                                                                                                                                                                                                                                                                                                                                                                         Q6TFC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8SEB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LaeA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                            RESULT 61
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  SHEWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Normark B.B., Jordal B.H., Farrell B.D.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme complex. CO I is the cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane (By similarity).
-!-SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
BMBL; AF18716: AAF04050.1; --
GO; GO:0019866; C:inner membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005739; C:mitcchondrial electron transport chain; IEA.
GO; GO:0005739; C:mitcchondrian; IEA.
GO; GO:0004129; F:cytcchrome-c oxidase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006109; P:eransport; IEA.
GO; GO:0006810; P:transport; IEA.
                                   SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
MEDLINE=2043737; Pubmed=10984043;
Stover C.K., Pham X.-Q.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E. W., Lorry S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Scolytidae, Coccotrypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00115; COXI; 1.
PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COXI; 1.
COPPER; Electron transport; Heme; Inner membrane; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6; DB 2; Length 331;
Pred. No. 1.2e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         331 AA; 37001 MW; EFBEAB77CF5FC750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome oxidase I (Fragment).
Coccotrypes advena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Prec. nc.
                                                                                                                                                                                                                                                                                                                                                               wplete proteome; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                    EMBL; AE004642; AAG05542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      30.08;
                                                                                                                                                                                                                                                                         opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            PIR; A83377; A83377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 WRWLRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WRWLRR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=105108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion
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0;

Gaps

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349 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palame crassimana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         4 SLWALG 9
                                                                  AF466963;
                                                                           AF466964;
                                                                                                                                                                        AF466974;
                                                                                    AF466965;
                                                                                              AF466966;
                                                                                                                 AF466968;
                                                                                                                                   AF466970;
                                                                                                                                             AF466971;
                                                                                                                                                      AF466972;
                                                                                                                                                               AF466973;
                                                                                                                                                                                           AF466976;
                                                                                                                                                                                                   GO:0019866;
                                                                                                                          AF466969;
                                                                                                                                                                                 AF466975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion.
                                                                                                       AF466967
                                                                                                                                                                                                                                                                                                                                      Transport.
NON_TER
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=COI;
                                                                                                                                                                                                                                                                                                                                                                                                                                            177
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Best Local 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palame.
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                                                                                                                         EMBL;
EMBL;
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EMBL;
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                                                                                                                                             EMBL;
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                                                                                              EMBL;
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                                                                                                                                                                                                   66
69
69
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                    inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; AF466956; AAL75529.1; -.
EMBL; AF466958; AAL75530.1; -.
EMBL; AF466959; AAL75531.1; -.
EMBL; AF466969; AAL75531.1; -.
EMBL; AF466969; AAL75531.1; -.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                   c + 2 H(2)O.
PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Chrysomeloidea, Cerambycidae, Lamiinae, Acanthocinini,
                                                                                          R EMBL, AF466957; AAL75330.1;

R EMBL, AF466956; AAL75531.1;

R EMBL, AF466969; AAL75531.1;

R EMBL, AF466969; AAL7533.1;

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0005746; C:intcednodrial electron transport chain; IEA.

GO; GO:0005746; C:intcochondrian; IEA.

R GO; GO:0005799; C:mitcochondrian; IEA.

R GO; GO:0006119; F:cytcothrome-c oxidase activity; IEA.

R GO; GO:006119; P:electron transport; IEA.

R GO; GO:006819; P:electron transport; IEA.

R GO; GO:006819; P:electron transport; IEA.

R Pfam; PF00115; COX1; 1.
                                                                                                                                                                                                                             PRINTS; PR01165; CYCOXIDASEI.
PROSTIES, PS00077; COX1, 1.
COPDET; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                  DB 2; Length 349; 1.3e+02;
                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                9E01675E32202D9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                           30.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Last annota Cytochrome oxidase subunit I (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                38997 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21.
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                       349
                                                                                                                                                                                                                                                                                                                                                                          177 SLWALG 182
                                                                                                                                                                                                                                                                                                349 AA;
                                                                                                                                                                                                                                                                                                                           Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=185376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        4 SLWALG 9
                                                                                                                                                                                                                                                                              1
349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palame mimetica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berkov A.;
                                                                                                                                                                                                                                                                    Transport
                                                                                                                                                                                                                                                                              NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                         O8SEE8
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Biol. J. Linn. Soc. Lond. 76:195-209(1002).
-- FUNCTION: Cytochrome c oxidase is the component of the respiratory
                                                 -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Acanthocinini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COXI; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0005746; C:mitochondrial electron transport chain; IEA. GO:0005739; C:mitochondrion; IEA. GO:0004129; F:cytochrome-c oxidase activity; IEA. GO:0006419; F:oxidoreductase activity; IEA. GO:0006118; P:electron transport; IEA. GO:0006118; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%; Score 6; DB 2; Length 349; 100.0%; Pred. No. 1.3e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38983 MW; 8DB95CDD99B03374 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
c + 2 H(2)O.
PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytochrome oxidase subunit I (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:inner membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                           EMBL; AF466961; AAL75534.1; -. EMBL; AF466962; AAL75535.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          AAL75542.1;
AAL75543.1;
                                                                                                                                                                                                      AAL75536.1;
                                                                                                                                                                                                                                        AAL75537.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL75545.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL75546.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL75547.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL75548.1;
                                                                                                                                                                                                                                                                    AAL75538.1;
                                                                                                                                                                                                                                                                                                                                   AAL75540.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL75549.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349
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Pfam; PF00115; COX1; 1
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InterPro; IPR000883; COX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00115; COX1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 SLWALG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6: Consert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palame crassimana.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=185373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkov A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=COI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8SEJ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8SEJ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 66
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Biol. J. Linn. Soc. Lond. 76:195-209(2002)
-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Bectrons originating in cytochrome c are transferred via the copper A center of subunit 2
chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Blectrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
                                                           and copper B (By similarity).

CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)0.
                                                                                                                                     inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                          PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Acanthocinini;
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00077; COX1; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                 G0:0019866; C:inner membrane; IEA.
G0:0016021; C:integral to membrane; IEA.
G0:0005746; C:mitochondrial electron transport chain; IEA.
G0:0005739; C:mitochondrion; IEA.
G0:0004129; F:cytochrome-c oxidase activity; IEA.
G0:0016491; F:oxidoreductase activity; IEA.
G0:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 6; DB 2; Length 349;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 AA; 39082 MW; 62579F8A877BF54A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.0%; Scc...
100.0%; Prev
0; }
                                                                                                                                                                                                                                                                                                                                  GO:0006810; P:transport; IEA
                                                                                                                                                                                            AF466953; AAL75526.1; -.
AF466954; AAL75527.1; -.
AF466955; AAL75528.1; -.
                                                                                                                                                               EMBL; AF466951; AAL75524.1; -. EMBL; AF466952; AAL75525.1; -.
                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01165; CYCOXIDASEI.
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000883; COXI.
Pfam; PF00115; COXI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 SLWALG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palame crassimana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=185373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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                                                                                                                                                                                                                                                                                                                                                                                                                                              349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SLWALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berkov A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=COI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08SEJ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O8SEJ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palame
                                                                                                                                                                                                                                    666666666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 65
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0;
and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
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Biol. J. Linn. Soc. Lond. 76:195-209(2002).

-!-FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons oxiginating in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Acanthocinin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PROIJÉS; CYCOXIDABBI.
PROSITE; PS00077; COX1; 1.
COPPer; Electron transport; Heme; Inner membrane; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.0%; Score 6; DB 2; Length 349; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 AA; 39089 MW; 5D199239F87C90E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence
05-JUL-2004 (TrEMBLrel. 27, Last annotati
Cytochrome oxidase subunit I (Fragment).
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membrane (By similarity)
                                                                                                                                       G0; G0:0005739; C:mitochondr.
G0; G0:0004129; F:cytochrome
G0: G0:0016491; F:cytochrome
G0; G0:0006118; P:electron t.
G0; G0:0006810; P:transport;
InterPro; IPR000883; COXI.
                                                         AAL75551.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             1
349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seminalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=185381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                           349
                                                            AF466978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                        Transport.
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=COI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sporetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sporetus
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08SKE5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8SKE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 68
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Biol. J. Lim. Soc. Lond. 76:195-209(2002).

-! FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Blectrons originating in catalytic subunit of the enzyme is lectrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and copper B (By similarity). CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
  cytochrome c are transferred via the copper A center of subunit 2 and heme A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                 inner membrane (By similarity).
SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c + 2 H(2)0.
PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Acanthocinin;
                                                                                     c + 2 H(2)O.
PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1165; CYCOXIDASEI.
PROSTRIS, PS00077; COX1, 1.
COPDET: Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                        GO:0019866; C:inner membrane; IEA.
GO:0016021; C:integral to membrane; IEA.
GO:0005739; C:mitochondrial electron transport chain; IEA.
GO:0005739; C:mitochondrion; IEA.
GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO:0016118; P:electron transport; IEA.
GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.0%; Score 6; DB 2; Length 349; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39075 MW; 5D068D39E76390E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
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100.08; Fi
                                                                                                                                                                                                               AF466940; AAL75513.1; -.
                                                                                                                                                                                          AF466939; AAL75512.1;
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000883; COX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 SLWALG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=185376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SLWALG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palame mimetica.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berkov A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=COI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8SEP8;
                                                                                                                                                                                          EMBL; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8SEP8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 67
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        SO PRESENTANT MEMORY COLOR COL
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-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family. BMBL; AF466981; AAL75554.1; -. GO; GO:0019866; C:inner membrane; IEA.
GO; GO:0010866; C:inner membrane; IEA.
GO; GO:00105746; C:integral to membrane; IEA.
GO; GO:0005746; C:mitochondrial alectron transport chain; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
L; AF466977; AAL75550.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Cerambycidae; Lamiinae; Acanthocinini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                              G0:0019966; C:inner membrane; IEA.
G0:0016021; C:inner membrane; IEA.
G0:0005735; C:intochondrial electron transport chain; IEA.
G0:0005739; C:mitochondrion; IEA.
G0:0004129; F:cytochrome-c oxidase activity; IEA.
G0:0016118; F:electron transport; IEA.
G0:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berkov A.;
"The impact of redefined species limits in Palame (Coleoptera
                                                                                                                                                                                                                                                                                                                                             Pfam, PF00115; COX1; 1.
BRNN'S; PR01165; CYCXIDASEI.
PROSITE; PS00077; COX1; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38978 MW; 2D3815E9B8B1AEEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.0%; Score 6; DB 2; Ler 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0;
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us-10-066-965a-1.oligo.rup

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Copper; Electron transport; Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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                                                                                                                                                                                                                                                177 SLWALG 182
                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=185386;
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                                                                                                                                                                                                             4 SLWALG 9
                                                              349
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                                          Transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=COI;
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                                                                                                                                                                                                                                                                                                                                                               QBSKE7;
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-!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Submits 1-3 form the functional core of the enzyme complex. CO I is the catalytic submit of the enzyme. Blectrons originating in cytochrome c are transferred via the copper A center of submit 2 and heme A of submit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Chrysomeloidea, Cerambycidae, Lamiinae, Acanthocinini,
                                                                                     PRINTS; PR01165; CXX1; 1.
PRINTS; PR01165; CXCOXIDASEI.
PROSITE; PS00077; CXX1; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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                                                                                                                                                                                                                                            39138 MW; BAB5303A8AB7926E CRC64;
GO; GO:0004129; F:cytochrome-c oxidase activity; IEA. GO; GO:0016491; F:oxidoreductase activity; IEA. GO; GO:0006118; P:electron transport; IEA. GO; GO:006810; P:transport; IEA. InterPro; IPR000881; COXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 AA
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PROSITE; PS00077; COX1; 1.
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Pfam; PF00115; COXI; 1.
                                                                                                                                                                                                                                                                                                  Local Similarity 100.
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                                                                                                                                                                                                                             349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oedopeza leucostigma.
                                                                                                                                                                                                                                              349 AA;
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                                                                                                                                                                                                           1
349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=COI;
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Biol. J. Linn. Soc. Lond. 76:195-209(2002).
-!-FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. CO I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and home A of subunit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Chrysomeloidea, Cerambycidae, Lamiinae, Acanthocinini,

    c + 2 H(2)O.
    -!- PATHWAY: Respiratory chain; terminal step.
    -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

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                                                                                                                                                      0;
                                                                                         30.0%; Score 6; DB 2; Length 349; 100.0%; Pred. No. 1.38+02; ive 0; Mismatches 0; Indels
349 349
349 AA; 38953 MW; 03815114721FABE9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome oxidase subunit I (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neoeutrypanus sp. AMNH-1806.
Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000883; COXI.
                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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DB 2; Length 349;

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232 SLWALG 237
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                                                                                                                                                                                                                                                                    xyleborus affinis.
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q8SHS2
ID Q8SHS2
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                                                                                      O9TAQ8
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                                  RESULT 73
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                                                                 29TAQ8
                                                                                                                           SOUTH THE REAL PROPERTY OF THE PROPERTY OF THE
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                                     Gaps
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MB4;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
Chan Y., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of the T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
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Bok J W., Keller N.P.;
"LaeA, a Regulator of Secondary Metabolism in Aspergillus spp.";
Eukaryotic cell 3:527-535(2004).
EMBL; AY422723; AAR01218.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 6; DB 2; Length 349;
Pred. No. 1.3e+02;
                                     Indels
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Complete protecome; HypotheLical protein.

SEQUENCE 349 AA; 40480 MW; 6556C185EC903F8B CRC64;
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14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                     ..
      Pred. No. 1.3e+02;
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                                  0; Mismatches
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100.08;
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                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=TTE0067;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                    SLWALG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLWALG 107
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      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=119072;
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                                                                                            4 SLWALG 9
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01-MAR-2004
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      Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAROLLI 72
AAROLLI B
D AAROLLI
AC AAROLL
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DT 18-API
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                                                                                                                                                                                                                                              RESULT 71
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Normark B.B., Jordal B.H., Farrell B.D.; DBJ databases.

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1999) to still as the component of the respiratory chain that catalyzes the reduction of oxygen to water. Submits 1-3 form the functional core of the enzyme complex. CO i is the catalytic subunit cost of the enzyme complex. CO i is the catalytic subunit conference of the enzyme comper A center of subunit 2 and heme A of submit 1 to the bimetallic center formed by heme A3 and copper B (By similarity).

-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Respiratory chain; terminal step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
-!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
EMBL; AF187138; AAF04072.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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PROSTIS: PS00077; COX1; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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G0:0016021; C:integral to membrane; IEA.
G0:0005739; C:mitochondrion; IEA.
G0:0005739; C:mitochondrion; IEA.
G0:0004129; F:cytochrome-c oxidase activity; IEA.
G0:0016118; P:electron transport; IEA.
G0:0006118; P:electron transport; IEA.
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                                                                                                                                                                                                                              Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Phytophaga, Scolytidae, Xyleborus.
NCBI_TaxiD=105120.
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352 AA
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Cytochrome oxidase subunit I (Fragment)
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01-JUN-2002 (TrEMBLrel. 21, Last seq
                                                            Created)
                                                      01-MAY-2000 (TrEMBLrel. 13, Creat

01-MAX-2000 (TrEMBLrel. 13, Last

01-MAR-2004 (TrEMBLrel. 26, Last

Cytochrome exidase I (Fragment).
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Mitochondrion.
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Job time : 95.5 secs
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0
                                                  inner membrane (By similarity).

FMILARITY: Belongs to the heme-copper respiratory oxidase family.

EMBL; AF444060; AAM12655.1; ---

GO, GO:0019866; C:inner membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016739; C:intcohondrial electron transport chain; IEA.

GO; GO:0005739; C:intcohondrian; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:000610; P:transport; IEA.

GO; GO:000610; P:transport; IEA.
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STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
MEDLINE=22022145; Prebro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
                                                                                                                                                                                                                PATHWAY: Respiratory chain; terminal step. SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1165; CYCOXIDASEI.
PROSITE; PS00077; COX1; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane;
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
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356 AA; 39160 MW; 4221CCBD0FA1DEA6 CRC64;
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24, Last annotation update)
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       Phytophaga; Scolytidae; Coccotrypes.
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01-JUN-2003 (TrEMBLrel.
GumG protein.
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RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., RA Faria U.B., Ferreira R.C.C., Ferro M.I.T., RA Faria U.B., Franco M.C., Greggio C.C., Gruber A., Ratsuyama A.M., Kishl L.T., Lette R.P., Lemos E.G.M., Lemos M.V.F., RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., RA Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., RA Martins E.C., Machado M.A., Tamura R.E., Teixeira E.C., Oliveira V.R., Oliveira M.C., Oliveira V.R., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., RA Schubal J.C., Kitajima J.P.;
RY "Comparison of the genomes of two Xanthomonas pathogens with differing R. Nature 417459-463 (2002).
BR EMBL; AE012356; AAM41726.1; -
BR GO, GO:0016747; Ertansferase activity, transferring groups o. ..; IEA. BR EMBL; AE012356; AAM1726.1; -
BR Therbro; IPR002656; Acyl transfe.
BR GO, GO:0016747; Ertansfe.
So SEQUENCE 356 AA, 39137 MW; D30COF7BIF40F3BA CRC64;

Query Match

Query Match

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Query Match

Past Local Similarity 100.0%; Pred. No. 1.38+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: October 26, 2004, 07:22:20
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Protein interaction; interaction trap; fusion protein; mimetic; therapeutic; detection; reporter gene.
                                          Interaction trap system aptamer 7.
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Abo16092 Human sec
Abo13798 Human sec
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nes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW32121 standard; peptide; 20 AA.
                                                                                                AAR89346 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 66; Page 60; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                             Jessen TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVWSLWALGWRWLRRYGWNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OVWSLWALGWRWLRRYGWNM
                                                                                                                                                                                                                                                                                                 95WO-US009307.
                                                                                                                                                                                                                                                                                                                       94US-00278082.
 9 9
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                           (GEHO ) GEN HOSPITAL CORP.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100."
1089
                                                                                                                                                                                                                                                                                                                                                                             Brent R, Mccoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-105852/11
30.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 AA;
                                                                                                                                                                                                                                                     WO9602561-A1
                                                                                                                                                                                                                                                                                                                       20-JUL-1994;
                                                                                                                                                                                                                                                                                                  20-JUL-1995;
                                                                                                                                                                                                                                                                            01-FEB-1996.
                                                                                                                                           10-SEP-1996
                                                                                                                                                                                                                                  Synthetic.
 9 9
                                                                                                                      AAR89346;
                                                                          RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW32121
ID AAW:
XX
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Aptamers AAW32116-W32132 have been isolated from a peptide library and are used in a novel interaction trap method for detecting protein interactions and isolating novel proteins. The method involves a host cell containing a reporter gene operably linked to a DNA-binding-protein (DBP) recognition site, a fusion gene capable of expressing a fusion protein which is able to specifically bind to the DBP recognition site and a second fusion gene which expresses a second fusion protein which is onformationally constrained and bonded to a gene activating moiety. Measuring expression of the reporter gene gives a measure of the interaction between Pl and P2. This method can be used to identify agonists or antagonists for use as therapeutic molecules or for the cissing of simple molecule mimetics. The method is specifically used to detect an interacting protein in a population of proteins or to identify a candidate interactor. Using conformationally constrained proteins can provide for terriary structural analysis and can also protect proteins from cellular degradation and/or increase the protein's solubility, and/or otherwise alter the capacity of the candidate interactor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
                                                                                                                                                                                                                                                                                                                                                                                                                         New trap system for detecting protein interactions - comprises a reporter gene linked to a DNA-binding-protein recognition site and fusion proteins to test for interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 2; Ls
100.0%; Pred. No. 4.4e-14;
Mismarches 0;
                                                                                                                                                                                                                                                                       Xu CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY49340 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 73; Page 52; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVWSLWALGWRWLRRYGWNM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OVWSLWALGWRWLRRYGWNM 20
                                                                                                                                                                                                                                                                       Jessen TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cdk2 interacting peptide i5-4.
97WO-US005793.
                                                                        96US-00630052.
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                                                                                                                                                 (GEMO ) GEN HOSPITAL CORP.
(GEMY ) GENETICS INST INC
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Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                   Brent R, Mccoy JM,
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Example 1; Fig 1; 33pp; English
 (MOLE-) MOLECULAR SCI INST.
                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                                       6 WALGWRWLRRYGW 18
                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                         6 WALGWRWLRRYGW
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                                       WPI; 2002-418829/45
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brent R,
                   Brent R,
                                                                                                                                                                                                                                                        Sequence 20 AA;
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                   Colas P,
                                                                                                                                                                                                                                                                                         Best Loca
Matches
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AAC18007
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                                                                                                                                                                                                                                                                           cells comprising recombinant DNA molecules encoding fusion proteins, each consisting of a candidate interactor peptide, a conformation-constraining protein and a DNA binding moiety and/or gene activating moiety. The cells are useful for detecting protein interactions. The cells may also be used in a method for identifying and purifying genes encoding a wide range of useful proteins based on their physical interaction with a second
                                                                                                                                                                                                               Population of Saccharomyces and/or mammalian cells comprising recombinant DNA encoding fusion proteins, useful for detecting protein interactions.
                                                                                                                                                                                                                                                                  The invention relates to a population of Saccharomyces and/or mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intracellular target; cellular component; property modulation; antimicrobial; immunomodulatory; noctropic; neuroprotective; metabolic; neurologic; cytostatic; cardiant; infection; immunological disorder; neurological disorder; metabolic disorder; psychiatric disorder; myopathy; cancer; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intracellular target molecule property modulation method aptamer 10M.
                                                                                                                                                                                                                                                                                                                                                                                                          0;
conformation-constraining protein; DNA binding moiety; Cdk2, gene activating moiety; protein interaction; gene purification
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 3; Length 20; 100.0%; Pred. No. 4.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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(MASS-) MASSACHUSETTS GEN HOSPITAL.
                                                                                                                                                                                                                                             Disclosure; Fig 3B; 24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVWSLWALGWRWLRRYGWNM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVWSLWALGWRWLRRYGWNM 20
                                                                                                                                                                     Jessen TH, Brent R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO18008 standard; peptide; 20
                                                                                              95US-00504538.
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                                                                                                                                     (GEMY ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                          20; Conservative
                                                                                                                                                                                         WPI; 2000-072059/06
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                Sequence 20 AA;
                                                                                             20-JUL-1995;
                                                                                                                  20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1205191-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2002
                                                    US6004746-A
                                                                         21-DEC-1999
                                                                                                                                                                       Mccoy JM,
                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intracellular target; cellular component; property modulation; antimicrobial; immunomodulatory; nootropic; neuroprotective; metabolic; neuroleptic; cytostatic; cardiant; infection; immunological disorder; neurological disorder; metabolic disorder; psychiatric disorder; myopathy; cancer; cardiovascular disorder.
                                                                                                                                                            Process for specifically modulating the properties of an intracellular target molecule used for the treatment of various disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Process for specifically modulating the properties of an intracellular target molecule used for the treatment of various disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intracellular target molecule property modulation method aptamer 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.0%; Score 13; DB 5; Length 20; 100.0%; Pred. No. 9.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO18007 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                      Example 1; Fig 1; 33pp; English.
Cohen BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-2000; 2000EP-00403156.
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(MASS-) MASSACHUSETTS GEN H
(MOLE-) MOLECULAR SCI INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
           The present invention relates to a process for specifically modulating the properties of an intracellular target molecule T, and/or of a cellular component C which interacts directly or indirectly in a cell with the target. The process involves the introduction into the cell of chimeric molecule known as a targeted effector, comprising a recognition moiety capable of recognising T and an effector moiety. The chimeric protein or nucleic acid can be used in the preparation of a medicament for the treatment of microbial infections, immunological disorders, myopathies, genetic disorders, metabolic disorders, psychiatric disorders, myopathies, genetic disorders and dental disorders. The present sequence is a known anti-Cdk2 aptamer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                      Length 17;
                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                    Score 12; DB 5; Le
Pred. No. 9.6e-06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 31470; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa polypeptide #14899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO82724 standard; protein; 480 AA.
                                                                                                                                                                                                                                                                                                        60.00,
100.08; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                               1 QVWSLWALGWRW 12
                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVWSLWALGWRW 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Local 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-615309/58.
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                                                                                                                                                                                                                                                                  Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      human, contractile rate; heart muscle; heat shock protein 20; HSP20; cardiac disorder; bradyarrhythmia; bradyardia; congestive heart failure; stunned myocardium; pulmonary hypertension; disortolic dysfunction; hypertension; anaemia; hyperthyroidism; pulmonary stenosis; protein therapy; antiarrhythmic; cardiant; hypotensive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Increasing the contractile rate in heart muscle, useful for treating e.g., congestive heart failure, heart muscle failure, pulmonary hypertension or bradyarrhythmia, comprises administering one or more heat
polypeptides of the invention. Note: The
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphoserine peptide analogue derived from HSP20 protein SegID 299.
                  sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Creazzo TL;
                                                                                                                                                           .;
                                                                                                                        Length 480;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Komalavillas P, Pipkin WJ, Johnston JA,
                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Phosphorylated serine"
                                                                                                                      Score 8; DB 7;
Pred. No. 2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIV ARIZONA STATE.
MEDICAL COLLEGE GEORGIA RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; SEQ ID NO 299; 116pp; English.
                                                                                                                          40.0%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  ADL14700 standard; peptide; 13 AA.
   represent P. aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-2003; 2003WO-US026366.
                                                                                                                                        100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2002; 2002US-0405199P,
21-FEB-2003; 2003US-0448953P,
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                           Conservative
                                                                                                                                                                                                                              262
                                                                                                                                                                                            8 LGWRWLRR 15
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                                                                                                                                        Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                              LGWRWLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shock protein 20
                                                                                       Sequence 480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004017912-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-2004
 AB084396
                                                                                                                                                                                                                                                                                                                                                     ADL14700;
                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDI-)
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         example, hypertension, anaemia, hyperthyroidism and pulmonary stenosis. Accordingly, these compositions can be used for protein therapy and sexhibit antiarrhythmic, cardiant and hypotensive activities. This peptide sequence is a phosphoserine peptide analogue derived from the human HSP20 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel polypeptide comprising a heat shock protein 20-derived polypeptide. A polypeptide of the invention has cytostatic, antiarteriosclerotic, vasotropic, antianginal, cerebroprotective, antiarrhyhmic, antiasthmatic, gynaecological, hypotensive, antimigraine, tocolytic, and relaxant activity, and may act as a HSP agonist or antegonist. The polypeptides, heat shock protein (HSP) 20, and methods are useful for treating or preventing a disorder, e.g. intimal hyperplasia, stenosis, restenosis, transplant vasculopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New heat shock protein 20-derived polypeptides, useful for inhibiting, treating or preventing smooth muscle cell vasospasm or a disorder such intimal hyperplasia, restenosis, atherosclerosis or smooth muscle cell
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      heat shock protein 20; cytostatic; antiarteriosclerotic; vasotropic; antianginal; cerebroprotective; antiarrhythmic; antiasthmatic; gynaecological; hypotensive; antimigraine; tocolytic; relaxant; HSP; smooth muscle cell; smooth muscle cell;
congestive heart failure in individuals suffering from, for
                                                                                                                                                                                                                                                                                                                                                                                                          HSP20 phosphopeptide analogue PTD-scrambled-pHSP20 SEQ ID NO:308.
                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lokesh J;
                                                                                                                                                                       0; Indels
                                                                                                                                          Length 13;
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                                                                                                                                        30.0%; Score 6; DB 8;
100.0%; Pred. No. 15;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; SEQ ID NO 308; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Phosphorylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                 ADH76207 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2002; 2002WO-US026918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001; 2001US-0314535P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Komalavilas P,
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOMALAVILAS P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV ARIZONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-393248/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PANITCH A.
                                                                                                                                                       Local Similarity
                                                                                                                                                                                                      SLWALG 9
                                                                                                                                                                                                                                 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BROPHY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003018758-A2
                                                                                                            Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEAL B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                             ADH76207;
                                                                                                                                          Query Match
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(SEAL/)
(LOKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYAR-)
(BROP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KOMA/)
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                 RESULT 8
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atherosclerosis, smooth muscle cell tumours such as leiomyosarcoma, ovasospasm, which is associated with angina, coronary vasospasm, Prinzmetal's angina, coronary ischaemia, stroke, bradycardia, hypertension, pulmonary (lung) hypertension, asthma (bronchospasm), toxemia of pregnancy, pre-term labour, pre-eclampsia/eclampsia, Raynaud's disease, Raynaud's phenomenon, haemolytic-uremia, non-occlusive mesenteric ischaemia, anal fissure, achaliasia, impocence, migraine, or ischaemic muscle injury associated with smooth muscle spasm. The polypeptides and HSP 20 are also useful for inhibiting smooth muscle cell broliferation and/or migration. The present sequence represents a peptide used in a polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New heat shock protein 20-derived polypeptides, useful for inhibiting, treating or preventing smooth muscle cell vasospasm or a disorder such intimal hyperplasia, restenosis, atherosclerosis or smooth muscle cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heat shock protein 20; cytostatic; antiarteriosclerotic; vasotropic; antianginal; cerebroprotective; antiarrhythmic; antiasthmatic; gynaecological; hypotensive; antimigraine; tocolytic; relaxant; HSP; smooth muscle cell; smooth muscle cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel polypeptide comprising a heat protein 20-derived polypeptide. A polypeptide of the invention cytostatic, antiarteriosclerotic, vasotropic, antianginal,
                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                      Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heat shock protein 20 analogue SEQ ID NO:305.
                                                                                                                                                                                                                     DB 7;
                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                     30.0%; Score 6; DB 7
100.0%; Pred. No. 26;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; SEQ ID NO 305; 194pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             ADH76204 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2002; 2002WO-US026918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BROPHY C.
KOMALAVILAS P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIV ARIZONA.
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 22
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                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                    4 SLWALG
                                                                                                                                                                                                                                                                                                                 SLWALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003018758-A2
                                                                                                                                                                                         Sequence 26 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                          ADH76204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LOKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BROP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PANI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SEAL/)
                                                                                                                                                                                                                                                       Matches
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                    hypotensive, antimigratine, trocolytic, and relaxant activity, and may act as a HSP agonist or antagonist. The polypeptides, heat shock protein (HSP) 20, and metchods are useful for treating or preventing a disorder, e.g. intimal hyperplasia, stenosis, restenosis, transplant vasculopathy, attherosclerosis, semoch muscle cell tumours such as leiomyosarcoma, or vasospasm, which is associated with angina, coronary vasospasm, prinzmetal's angina, coronary ischaemia, stroke, bradycardia, hypertension, pulmonary (lung) hypertension, asthma (bronchospasm), toxemia of pregnancy, pre-term labour, pre-eclampsia/eclampsia, Raynaud's disease, Raynaud's stroke, and processed to the strong coronary in the modition of the strong coronary is a stroke, and a stroke colusive and the strong coronary is a stroke, and a stroke colusive and the strong coronary is a stroke colusive and column 
                                                                                                                                                                                                                                                                                                                   mesenteric ischaemia, anal fissure, achalasia, impotence, migraine, or ischaemic muscle injury associated with smooth muscle spasm. The polypeptides and HSP 20 are also useful for inhibiting smooth muscle cell
                                                                                                                                                                                                                                                                                                                                                                                                       iferation and/or migration. The present sequence represents a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypethysoidism; cholesterol ester storage disease; immune deficiency; immune disorder; inflectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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     cerebroprotective, antiarrhythmic, antiasthmatic, gynaecological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                  used in a polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.0%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP08236 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US010836.
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29-AUG-2000; 2000US-0228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets RA, Leach MD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-106308/14.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29 AA;
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

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treating given in ABPRONIC to ABPRILEGO. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, near the transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid airsease autoimmune thyroidistis, mysethenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                               useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide designated ORFX are present in human atherogenic cells are useful to prevent and treat ORFX-associated disorders including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet; human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder.
specification). ABN15762 to ABN27252 encode the human ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.0%; Score 6; DB 5;
100.0%; Pred. No. 45;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2001; 2001US-00867550.
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Best Local Similarity 100.
Matches 6; Conservative
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CONLEY P B.
TOPPER J N.
LAW D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 QVWSLW 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABQ99000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OVWSLW
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORF807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP64437;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                        The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631-ABP64681 and ABQ98194-ABG99267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood for this patent did not form part of the printed specification, but was sequate uspto.gov/sequence.html?DocID=20020082206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a prophylaxis and treatment of pathological conditions resulting from a prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 112;
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... 0; Mismatches
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                                                                                                   Claim 10; SEQ ID NO 1614; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABO84088 standard; protein; 138 AA.
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98US-0094190P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112 AA;
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ABO84088
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including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-Sequence represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynocleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences ABO4302 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed appearance may be a peruginosa polypeptides of the invention. Note: The specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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100.0%; Pred. No. 96;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa polypeptide #10247.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO78072 standard; protein; 171 AA.
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                                                                                                                                                           seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                               6; Conservative
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N-PSDB; ABD11643.
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Best Local Similarity
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                                                                                                                                                                                                   Sequence 138 AA;
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27-JUL-1998;
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Matches
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seqdata.uspto.gov/sequence.html

ADM26747;

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Matches

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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a barcherial infection, for evaluating a compound, such as a polypeptide, or for the ability to bind a P. aeruginosa mucleic acid, as components of effective antibacterial targets, as templates for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant or production of P. aeruginosa drugs, as templates for recombinant of P. aeruginosa sequences or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences of Pseudomonas species using biochip technology. Sequences ABO67826-Capacidication and in detection of P. aeruginosa sequences ABO67826-Capacidication but was obtained in electronic format from USPTO at sequence. ABO8436 represent P. aeruginosa polypeptides of the printed specification but was obtained in electronic format from USPTO at sequence. ABO8436 represent P. seruginosa polypeptides of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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                                                                                                                                  Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Bush
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100.0%; Pred. No. 1.6
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel central nervous system protein #13.
                                                                                             Pseudomonas aeruginosa polypeptide #996.
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100.0%; FIL
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98US-0094190P.
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Best Local Similarity luv.
6; Conservative
                                                                                                                                                                          Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Rubenfield MJ,
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                  ABO68821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acids encoding any of about 1700 Methanopyrus kandleri proteins, and the encoded proteins, useful as a medicaments or as diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                               Gaps
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                                                        Length 171;
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                                                                                                                                                                                                                                                                                                                                                                                       Hyperthermophile Methanopyrus kandleri protein #1353.
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                                                      DB 7; Len
                                                                                                                                                                                                                                                                                                                                                                                                                              hyperthermophile; protein stability enhancement;
                                        30.0%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
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2002US-0380423P.
2002US-0410974P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                protein activity enhancement
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                                                                                               6; Conservative
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                    Sequence 171 AA;
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16-SEP-2002;
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(FIDE-) (MALY/)

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RESULT 15

ABO68821 ID ABO6

Best Loc Matches

cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; resticular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy. 2000US - 0227182P 2000US - 0227099P 2000US - 0228934P 2000US - 0229343P 2000US - 0229344P 2000US - 0229344P 2000US-0229509P 2000US-0229513P 2000US-0230437P 2000US-0231242P 2000US-0231243P 2000US-0231243P 2000US-0231414P. 2000US-0232081P. 2000US-0232081P. 2000US-0232397P. 2000US-0232398P. 2000US-0232398P. 2000US-0232399P. 2000US-0225267P 2000US-0225268P 2000US-022540P 2000US-022547P 2000US-0225757P 2000US-0225758P 2000US-0179065P. 2000US-0180628P. 2000US-0184664P. 2000US-0189874P. 2000US-0190076P. 2000US-019131P. 2000US-0205515P. 2000US-0214886P. 2000US-0215135P. 2000US-0216647P. 2000US-0216880P. 2000US-0217487P. 2000US-0217496P. 2000US-0220963P. 2000US-0220964P. 2000US-0224518P. 2000US-0224519P. 2000US-0225213P. 2000US-0225214P. 2000US-0225266P. 2000US-0226681P. 2000US-0226868P. 2000US-0231413P 2000US-0218290P 2000US-0226279P. 17-JAN-2001; 2001WO-US001332 WO200155318-A2 11-SEP-2000; 201-SEP-2000; 201 31-JAN-2000; 04-FEB-2000; 02-FEB-2000; 02-MAR-2000; 11-MAR-2000; 11-AAR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 28-JUN-2000; 07-JUN-2000; 07-JUN-2000; 07-70L-2000; 11-70L-2000; 14-70L-2000; 26-70L-2000; 26-70L-2000; 14-AUG-2000; 18-AUG-2000; 22-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000; 14-SEP-2000; 214-SEP-2000; 214 Homo sapiens 02-AUG-2001

2000US-0233064P 2000US-0233064P 2000US-0234223P 2000US-023423P 2000US-023493P 2000US-023493P 2000US-0235884P 2000US-0235884P 2000US-02358836P 2000US-02358836P 2000US-02358836P 2000US-02358836P 2000US-02358836P 2000US-0235836P 2000US-0235836P 2000US-0235836P 2000US-0236369P 2000US - 0241221P 2000US - 0241785P 2000US - 0241787P 2000US - 0241787P 2000US - 0241803P 2000US - 0241803P 2000US - 0241826P 2000US - 0241826P 2000US - 024617P 2000US - 0246474P 2000US-0246478P.
2000US-0246523P.
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2000US-0249211P. 2000US-0249216P 2000US-0249217P 2000US-024924PP 2000US-0249245P 2000US-0249245P 2000US-0249265P 2000US-0249265P 2000US-0249265P 2000US-024929P 2000US-024929P 2000US-0237038P. 2000US-0237039P. 2000US-0237040P. 2000US-0239935P. 2000US-0239937P. 2000US-0246476P 2000US-0246477P 2000US-0250391P 2000US-0256719P 2000US-0251479P 25.58P-2000; 27.58BP-2000; 29.58BP-2000; 29.58BP-2000; 29.58BP-2000; 29.58BP-2000; 29.58BP-2000; 20.50BP-2000; 20. 14-SEP-2000; 214-SEP-2000; 214-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-20-0CT-2000; 01-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; L7-NOV-2000; L7-NOV-2000; L7-NOV-2000; L7-NOV-2000;

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2000US-0232398P
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                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative clasorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. crebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. testicular feminisation, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. and pituitary dwarfism, cancers and disorders at the cellular level e.g. respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. caute kidney failure and blood related disorders e.g. mylocardial continental cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues to regenerate tissues and in chemorasis. The
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                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiparasitic; muscular; gynaecological; gastrointestinal; respiratory; cardiovascular-; antiarteriosclerotic; antiarrhythmic; cardiant; nephrotropic; litholytic; cytostatic; gene therapy; neural disorder; Alzheimer's disease; Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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nes 0; Indels
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100.0%; Pred. No. 1.8
tive 0; Mismatches
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08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251986P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-025190P.
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                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia; inflammatory disorder; ischaemia-reperfusion injury; inflammatory bowel disease; Crohn's disease; infectious disease; HIV infection; hepatitis infection; bacterial infection; fungal infection; parasitic infection; muscular disorder; pulmonary disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; atheroselerosis; arrhythmia; myocarditis; renal disorder; acute glomerulonephritis; pyelonephritis; renal lithiasis; proliferative disorder; cancerous diseases; human.
immune system disorder; diabetes; rheumatoid arthritis;
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2000US-022526P
2000US-0225267P.
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2000US-0226279P.
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2000US-0229343P.
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2000US-0230438P.
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2000US-0232397P.
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2000US-0256719P

05-DEC-2000;

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02-0CT-2000; 2000US-0237039F.
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17-NOV-2000;
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cardiovascular disorder; ischaemic heart disease; asthma; precured myocardial infarction; respiratory disease; asthma; precumonia; acute myocardial infarction; respiratory disease; asthma; precumonia; cystic fibrosis; chronic renal failure; glomerulopathy; gastrointestinal disorder; peptic ulcer; cirrhosis; immune disorder; my fir infection; system; clupus erythematosus; endocrine system; my diabetes mellitus; epilepsy; Alzheimer's disease; amyotropic lateral scierosis; skin disorder; psoriasis; bacterial; myotropic lateral scierosis; skin disorder; psoriasis; bacterial; fungal; parasitic; viral infection; cytostatic; antiasthmatic; antianeamic; cardiant; vasotropic; antiasthmatic; antiallergic; dermatological; antirheumatic; municipallergic; dermatological; antirheumatic; antisoriatic; antisoneumic antisoneumic incurporocective; nootropic; antipsoriatic; antibacterial; fungicide; antiparasitic; virucidal; my gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated polypeptide comprising an amino acid sequence at least 90% identical to: a polypeptide fragment, domain, epitope, or full-length protein of any one of 60% amino acid sequences (I) described in the specification, a polypeptide fragment of (I), or the encoded sequence contained in (II), having biological activity; or a variant, allelic variant, or a species homologue of (I). The polypeptides and nucleic acid molecules are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions with a neural disorders, e.g. Alzhaimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis, immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic
                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides and nucleic acid molecules, useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions e.g. neural disorders, reproductive disorders or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.0%; Score 6; DB 8; Led 100.0%; Pred. No. 1.8e+02; Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 621; 413pp; English.
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                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM, Barash SC;
             06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-025199P.
11-DEC-2000; 200US-025199P.
05-JAN-2001; 200UUS-025409P.
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N-PSDB; ADI53820.
                                                                                                                                                                                                                 (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 WLRRYG 221
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Sequence 335 AA;

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This invention relates to novel isolated human polynucleotides and the encoded proteins thereof. Specifically, it refers to proteases, kinases, phosphatases, secreted and transmembrane proteins, as well as the derived peptide fragments, which can be used to develop antibodies and screen for small molecule agonists and antagonists that can modulate their activities. The present invention describes polypeptides, polymbolecides, vectors and nate calls useful for diagnosing, preventing and treating proliferative disorders, e.g. cancer, disorders of the mematopoiesis such as thrombosis and natemia, cardiovascular disorders, e.g. ischaemic heart disease and anemia, cardiovascular disorders, e.g. ischaemic heart disease and anemia, cardiovascular disorders, e.g. extrointestinal disorders, e.g. chronic renal failure and glomerulopathy, gastrointestinal disorders, e.g. chronic renal failure and glomerulopathy, disorders, e.g. HIV infection and systemic lupus erythematosus, disorders disorders, e.g. diabetes mellitus, central nervous system disorders, e.g. poptic ulcer or cirrhosis, immune construction, expirations and system disorders, e.g. provinces mellitus, central nervous system disorders, e.g. postiasis, as well as bacterial, fungal, parasitic and viral diseases. Accordingly, they exhibit many various activities including cytostatic, anticoagulant, thrombolytic, anticoadulant, cardiant, vascironic immatory, contractive contractions and cardiant contractions disconders, e.g. entital diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nephrotropic, antiulcer, hepatotropic, immunosuppressive, antiallergic, defamatological, antirheumatic, antiathritic, antidiabetic, anticonvulsant, neuroprotective, noorropic, antipsoriatic, antibacterial, fungicide, antiparasitic and virucidal, such that these polynucleotides
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2002US-0406640P.
2002US-0406655P.
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2002US-0410953P.
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2002US-0410946P.
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2002US-0411024P.
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2002US-0406612P
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N-PSDB; ADM90746, ADM91164.
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RIKEN INST
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17-SEP-2002; 2
17-SEP-2002; 2
17-SEP-2002; 2
17-SEP-2002; 2
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29-AUG-2002;
29-AUG-2002;
17-SEP-2002;
17-SEP-2002;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                 Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database global search for G protein-coupled receptors, proteins and encoded genes for studying in vivo signal transduction mechanism and
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Length 335;
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                               Indels
                                                                                                                                                                                                                                                                                                                    drug development; gustatory; taste; fragrance; receptor.
DB 8; Ler
                               0; Mismatches
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identifying targets for drug development.
 Score 6; I
Pred. No.
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                                                                                                                                                                                                                                                                     Human GPCR polypeptide SEQ ID NO 4.
                                                                                                                                                                         ABP95597 standard; protein; 368 AA.
30.0%;
100.0%;
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                               Conservative
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                                                                                             194 SLWALG 199
Query Match
Best Local Similarity
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                                                              4 SLWALG
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                                9:
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Matches
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91

WLRRYG

98

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RESULT 20

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New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a new isolated nucleic acid encoding a Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regularory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 7940; 932pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU19932 standard; protein; 396 AA.
                                                                                    (GENO-) GENOME THERAPEUTICS CORP
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                 99US-0117747P.
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Thes 6; Conservative
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                                                                                                                                          Osborne M;
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Trawick JD,
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N-PSDB; ACH94974.
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06-MAR-2002;
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                                                                                                                                          GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU19932;
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELIT-)
                                                                                                                                             Breton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU19932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virtually all of the segment of Xanthomonas campestris DNA that contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA prodn. of xanthan gum or its variants - by transforming host cells with vector contg. DNA coding for enzymes involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a gene cluster that directs Xanthan biosynthesis (AAN70753), codes for protein products. Each gene is designated by a letter (see Fig 11) and its protein product is designated by that letter preceded by 'gp' (AAP70455-67). (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                      segment of Xanthomonas campestris DNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                contains a gene cluster that directs Xanthan biosynthesis.
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                                                                                                                                                                                                                                                                                                   Thickening agent; oil recovery; drilling fluid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capage MA, Doherty DH, Betlach MR,
                               AAP70461 standard; protein; 379 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO61423 standard; protein; 395 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87WO-US000604
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87US-00029530.
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                                                                                                                                                                                                                      Sequence of gpG encoded by
                                                                                                                                       (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polysaccharide synthesis.
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                                                                                                                                                                                                                                                                                                                                                     Kanthomonas campestris
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Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1987-291651/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-1986;
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                                                                                                                                    25-MAR-2003
13-FEB-1991
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                                                                                 AAP70461;
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AAP70461
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Carr GJ;

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Klebsiella pneumoniae.
                                                                                                            Local Similarity
                                                                                                                     7 ALGWRW 12
                                                                                                   Sequence 396 AA;
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22-DEC-2000; 2
16-FEB-2001; 2
                                                                                                                                                                                                        26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                   21-MAR-2000;
                                                                                                                                                                                                      23-MAY-2000;
                                                                                                                                                      14-FEB-2002
                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                AAU36106;
                                                                                                         Query Match
                                                                                                               Matches
                                                                                                                                    RESULT 23
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, consectul for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify correct or proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for homologous culcier acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                          Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%; Score 6; DB 4; Length 409; 100.0%; Pred. No. 2.2e+02; cive 0; Mismatches 0; Indels
                                                          Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                            Example 3; SEQ ID NO 11699; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #14206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG14215 standard; protein; 426 AA.
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23-AUG-2000; 2000US-00649167.
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                                                             Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
(ELIT-) ELITRA PHARM INC.
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                                                                                      Xu HH;
                                                                                                                                                2001-611495/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 409 AA;
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                                                                                                                                                                               N-PSDB; AAS53965
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                                                       Haselbeck R,
Yamamoto RT,
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                                              the invention traders to an institute and any other of the nucleic acid inhibits proliferation of a cell. Also included are:

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense contisense mucleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an equired for proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising strains in which the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound strains; or (13) identifying the target of a compound that inhibits the extent or organism; or (13) identifying the target of a compound that inhibits the compound section of an organism; or (13) identifying the target of a compound that inhibits or compound that inhibits or compound that inhibits or compound that inhibits or compound the compound that inhibits the compound compound that inhibits or compound the compound that inhibits or compound that inhibits or co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                 The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.0%; Score 6; DB 6; Length 396; 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klebsiella pneumoniae cellular proliferation protein #94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Preu. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU36106 standard; protein; 409 AA.
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2000US-0206848P.
2000US-02072P.
2000US-0242578P.
2000US-0253625P.
2000US-0257931P.
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Gaps

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ADH87525 standard; protein; 439 AA.
                                                                                                                                                                              Noucette-Stamm LA,
                                                                                                                                       antibacterial
                                                                                                                                                           13-AUG-1998;
                                                                                                                                                                15-AUG-1997;
                                                                                                                         22-APR-2004
                                                                                                                                                 JS6617156-B1
                                                                                                                                                      09-SEP-2003
                                                                                                                    ADH87525;
                                                                                   Query Match
                                                                                                                                                                      (DOUC/)
                                                                                                                                                                        BUSH/)
                                                                                        Matches
                                                                                                          RESULT 25
                                                                                                             ADH8752
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in fissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic manno acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO at
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 44574; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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. 0 30.0%; Score 6; DB 4; Length 426; 100.0%; Pred. No. 2.3e+02; 0; Indels 100.0%; Pred. No. 2.-6; Conservative Best Local Similarity Sequence 426 AA;

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Gaps

RESULT 26 AB068883

Enterococcus faecalis polypeptide #2005. (first entry)

Enterococcus faecalis infection; transcription regulatory element;

Enterococcus faecalis

98US-00134000,

97US-0055778P

DOUCETTE-STAMM L A. BUSH D. Bush D;

WPI; 2003-895394/82, N-PSDB; ADH84120.

New nucleic acid comprising a sequence encoding an Enterococcus fecalis

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polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Entercoccocus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                              The invention relates to Enterococcus faecalis polynucleotides and
  or
polypeptide, useful for preparing a composition for diagnosing treating E. fecalis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               30.0%; Score 6; DB 7; Len
100.0%; Pred. No. 2.4e+02;
iive 0; Mismatches 0;
                                                                  SEQ ID NO 5410; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
Les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 SLWALG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 439 AA;
                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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    # # X & X O O O O O O O O O O O X & O
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Bacterial infection; Pseudomonas aeruginosa infection; antibacterial. Pseudomonas aeruginosa polypeptide #1058. ABO68883 standard; protein; 445 AA. 98US-0074788P. (first entry) Pseudomonas aeruginosa. JS6551795-B1 18-FEB-1999; 18-FEB-1998; 27-JUL-1998; 29-JUL-2004 22-APR-2003

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection. WPI; 2003-615309/58. N-PSDB; ABD02454.

Bush D;

Deloughery C,

Nolling J,

Rubenfield MJ,

(GENO-) GENOME THERAPEUTICS CORP.

Disclosure; SEQ ID NO 17629; 455pp; English.

The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target

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Gaps

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Length 478; Indels

30.0%; Score 6; DB 7 100.0%; Pred. No. 2.5 :ive 0; Mismatches

Query Match Best Local Similarity luv.

443 WRWLRR 448

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15

WRWLRR

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components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826 AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                    DB 7; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                        100.0%; Preq. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa polypeptide #5507.
                                                                                                                                                                                                                                                                                                                 30.0%; Score 6; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO73332 standard; protein; 478 AA.
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
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N-PSDB; ABD06903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SLWALG 9
                                                                                                                                                                                                                                                          Sequence 445 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                    Query Match
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ABO73332
ACC ABO7332
ACC ABO732
ACC ABO
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Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal microlides; arachnid; nematode; insect; polyketide; polyketide synthase; PKS; extender module; initiator module; acyl transferase domain, AT; acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR; dehydratase domain; DH; encyl reductase domain; ER; beta-ketoreductase; insecticide;

SpnO protein involved in spinosyn biosynthesis.

(first entry)

01-DEC-1999

AAY39311;

AAY39311 standard; protein; 486 AA.

RESULT 28 AAY3931.

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This is the amino acid sequence of the product of the spnO gene. The protein is involved in spinosyn biosynthesis. The SpnO gene is one of 23 genes and open reading frames contained in an 80kb DNA sequence AAZ21501. Spinosyns are insecticidal microlides which are useful for the control of arachnids, nematodes and insects. Biosynthesis of spinosyns occurs via stepwise condensation and modification of carboxylic acid precursors generating a linear polyketide which is modified further. The DNA sequence contains a central region of approximately 55kb which has homology to the DNA encoding the polyketide synthases (PKS) of known macrolide producers. The spinosyn PKS DNA region consists of 5 ORFs with stop codons at the end of acyl carrier protein (ACP) domains. Together the PKS polypeptides (AAY3929-Y39301), form a complex consisting of an initiator module, sppA, and several extender modules spnB-spnE. The cintiator module, spnA, and several extender modules spnB-spnE. The products of the genes present in the region upstream of the PKS genes have been assigned names spnF-spnS AAX3302-Y39315 and are responsible considered that GPR-139317, and two ORFS ORFI and ORFL16 present immediately upstream of spnS, producing colypeptides AAY39316-Y39317, and two ORFS ORFI and ORFL16 present immediately upstream of spnS, producing spinosyn biosynthesis. The genes are useful to improve yields of spinosyns, and for creating new spinosyns e.g. by mutagenesis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 159-161; 190pp; English.
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as polypeptide, or the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant or production of P. aeruginosa derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences or cother sequences of Pseudomonas species using biochip technology. Sequences AB067826-CTC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence. The sequence data for this patent did not form part of the printed sequence. The sequence them

Sequence 478 AA;

New spinosyn biosynthetic genes from Saccharopolyspora spinosa, useful

for production of insecticidal spinosyn compounds

Crawford KP, Madduri K, Merlo DJ; Waldron C;

LLC.

(DOWC) DOW AGROSCIENCES Baltz RH, Broughton MC, Treadway PJ, Turner JR,

WPI; 1999-551414/46.

N-PSDB; AAZ21501

99WO-US003212.

16-FEB-1999; 09-MAR-1998;

16-SEP-1999

Saccharopolyspora spinosa.

WO9946387-A1.

dideoxysugar synthesis.

us-10-066-965a-1.oligo.rag

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Gaps

0;

0; Indels

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This invention describes a novel method muches acid (1) and its encoded activity involved in biosynthesis of spinosyns. (1) are used (1) to activity involved in biosynthesis of spinosyns. (1) are used (1) to identify, inactivate or medulate genes involved in the biosynthesis of identify, inactivate or medulate genes involved in the biosynthesis of adding forosamine or trimethylthamnose to a spinosyn or polyketide adding forosamine or trimethylthamnose to a spinosyn or polyketide aglycone, and (1) for recombinant production of the corresponding anymes, which are used for production of (11), their precursors or derivatives, including production of transgenic plants that express (11) and thus have increased resistance to insects. (1) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (11) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying also be used to raise specific antibodies useful for identifying cypression clones in a gene bank. Cells transformed with (1) may produce (11) at significantly increased levels or produce new derivatives of (11). This sequence represents an S. spinosa 2,3-dehydratase
interruption of steps in spinosyn biosynthesis. The modified spinosyns may be a new insect control agent or serve as substrates for further chemical modification and the creation of new semi-synthetic spinosyns. The genes are also useful to isolate similar sequences from S. spinosa or other species by hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method nucleic acid (I) and its encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forosamine; trimethylrhamnose; polyketide synthase; biosynthesis; spinosyn; polyketide aglycone; transgenic plant; insect resistance; macrolide; insecticidal; 2,3-dehydratase.
                                                                                                                                                                         DB 2; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. spinosa protein fragment encoded by ORF10, SEQ ID 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salas JA;
                                                                                                                                                                         30.0%; Score 6; DB 2
100.0%; Pred. No. 2.5
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 47; Page 139-140; 354pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                              AAB70957 standard; protein; 486 AA.
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                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-267102/28.
                                                                                                                                                                                                                                                                                                  480 SLWALG 485
                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                             4 SLWALG 9
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                                                                                                                                    Sequence 486 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2001
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                                                                                                                                                                             Query Match
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AAB70957
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30.0%; Score 6; DB 4; Length 486;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel DNA molecule comprising a DNA sequence that encodes a butenyl-spinosyn biosynthetic enzyme, a butenyl-spinosyn PKS (polyketide synthetase) domain, or a spinosyn PKS module. The butenyl-spinosyn biosynthetic genes are useful for increasing the production of butenyl-spinosyn insecticidal macrolides. The genes are also useful for an engage the metabolites or produces produced by spinosyn-producing microorganisms. The present sequence represents one of the butenyl-spinosyn biosynthetic polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New butenyl-spinosyn biosynthetic genes, useful for increasing the production of butenyl-spinosyn insecticidal macrolides, or for changing the metabolites or products produced by spinosyn-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                     Butenyl; biosynthetic enzyme; PKS; polyketide synthetase; macrolide;
                                                                                                                                                                                                                                        Saccharopolyspora busO butenyl-spinosyn biosynthetic gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bullard BS, Gustafson GD, Waldron C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 6; DB 6; Length 486;
100.0%; Pred. No. 2.5e+02;
iive 0; Mismatches 0; Indels
                Indels
 Pred. No. 2.5e+02;
Mismatches 0;
                0; Mismatches
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                                                                                                                                                   ABP57692 standard; protein; 486 AA.
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100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001US-0280175P.
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                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jackson JD,
                                                                                                                                                                                                                                                                                      metabolite; spinosyn.
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                                                                      480 SLWALG 485
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 Best Local Similarity
Matches 6; Conserv
                                              4 SIMALG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 486 AA;
                                                                                                                                                                                                                                                                                                                                              WO200279477-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitchell JC;
                                                                                                                                                                                                              22-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2002
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ABO61738
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                                                                                                                        RESULT 30
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The present invention relates to a method of producing a transformed plant that selectively increases production of gamma-aminobutryic acid (GABA) in response to a signal, by incorporating into the plant's genome a DNA construct with a non-constitutive promoter operably linked to a polynucleotide encoding a functional plant glutamic acid decarboxylase (GAB), to provide a transformed plant texpresses the GAB coding sequence in response to a signal, Plants of this type have an enhanced
                                                                                                                                                                                                  invention relates to identifying target proteins (ABB90790-ABB94016)
                                                                                                                                                                                                                  for herbicidally active compounds, comprising aligning and comparing muclaic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant organisms using suitable search parameters, where plant sequences having an B-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Making transformed plants that selectively increase gamma-aminobutyric acid production, by incorporating a DNA construct with a polynucleotide encoding a plant glutamic acid decarboxylase enzyme into plant's genome.
                                      Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAD; plant GABA production regulation; glutamic acid decarboxylase; plant stress; GABA; gamma-aminobutyric acid; stress resistance.
                                                                                                                                                    Claim 5; SEQ ID NO 2732; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.0%; Score 6; DB 5; Length 502; ilarity 100.0%; Pred. No. 2.6e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EMER -) EMERALD BIOAGRICULTURE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA015132 standard; protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 53; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001; 2001WO-US047447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2000; 2000US-0246367P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-490073/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRRYGW 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LRRYGW 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAL43410.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A thaliana GAD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200238736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinnersley AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                             herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA015132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element, and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nseful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                           Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a Klebsiella pneumoniae polypeptide, preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 6; DB 7; Length 493;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicidally active polypeptide SEQ ID NO 2732.
                  Klebsiella pneumoniae polypeptide segid 8255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, SEQ ID NO 8255; 932pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB93521 standard; protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                             27-JAN-2000; 2000US-00489039.
                                                                                                                                                                                                                                                                                                      99US-0117747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001; 2001WO-EP009892
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nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Osborne M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weidler M;
                                                                                                                         Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-895346/82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SLWALG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ACH95289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200210210-A2
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                                                                                                                                                                         US6610836-B1
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                                                                                                                                                                                                                                                                                                                                                                                           Breton GL,
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ò g RESULT 32 ABB9352: ABB93521;

Query Match

SO CCC CCC CCC X A X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A X X A

0

Gaps

0

isolated twenty-one induced gene fragments. This sequence is a partial sequence of the transcription factor encoded by open reading frame (ORP) 1 of the picric acid degredation cluster (See GENESEQ record AAA53941). (Updated on 12-SEP-2003 to standardise OS field)

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ability to tolerate environmental or other stresses. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Differential display method using a large number of arbitrary primers for RT-PCR used to isolate novel differentially expressed prokaryotic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A new method to identify differentially expressed prokaryotic genes using
                                                                                                                                                                                                                                                               Identification; prokaryote; polymerase chain reaction; PCR; amplification; primer; differential display; picric acid degredation; gene cluster; open reading frame; ORF; dehydratase; dehydrogenase; transcription factor; Acyl-CoA synthase; NADPH oxidoreductase.
                                                                         Gaps
                                                                          0;
                                           DB 5; Le.s.
No. 2.6e+02;
0; Indels
                                                  Score 6; DB 5; Pred. No. 2.6e
                                                                                                                                                                                                                                           Transcription factor partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 46-47; 66pp; English.
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             /note= "Gln or Glu"
                                                                                                                                                                  AAB02079 standard; protein; 532 AA.
                                                                                                                                                                                                                                                                                                                   Rhodococcus erythropolis; HL PM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ы
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DUPO ) DU PONT DE NEMOURS & CO
         is the A. thaliana GAD1 protein
                                                  30.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-2000; 2000WO-US003989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0120702P
                                                                                                                                                                                                             (revised)
(first entry)
                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-587069/55.
                                                                                                                395 LRRYGW 400
                                                Query Match
Best Local Similarity
                                                                                           13 LRRYGW 18
                               Sequence 502 AA;
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                                                                                                                                                                                                                                                                                                                                          Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                 WO200049177-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-1999;
                                                                                                                                                                                                            12-SEP-2003
03-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rouviere P;
                                                                                                                                                                                        AAB02079;
                                                                      Matches
                                                                                                                                                 RESULT 34
                                                                                                                                                         AAB02079
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                                                                                                                                                                                                                                                                                                                                                             Rhodococcus picric acid degradation pathway-related transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid fragments encoding enzymes of the picric acid degradation pathway isolated from Rhodococcus erythropolis HL PM-1, useful in the creation of recombinant organisms that have the ability
                                                                                                                                  Gaps
                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                         Picric acid degradation gene cluster, recombinant organism, picric acid degradation pathway, transcription factor.
                                                                                                    Score 6; DB 3; Length 532;
Pred. No. 2.7e+02;
0; Mismatches 0; Indels
                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 23-24; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
Misc-difference 532
                                                                                                                                                                                                                                                                   AA015193 standard; protein; 532 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Russ R;
                                                                                                       30.00
100.08; Fre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-2000; 2000US-00651941.
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                                                                                                    30.0%;
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rouviere PE, Walters DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodococcus erythropolis.
                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROUV/) ROUVIERE P E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WALTERS D M.
RUSS R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-381946/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor
                                                                                                                                                                                           332 SLWALG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degrade picric acid
                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                             4 SLWALG 9
                                                                        Sequence 532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAL43620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002042117-A1
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                                                                                                                                                                                                                                                                                                   AA015193;
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(RUSS/)
                                                                                                                                                                                                                                       RESULT 35
                                                                                                                                                                                                                                                       AA015193
888888
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Sequence 532 AA;

a large number of arbitrarily primed polymerase chain reactions comprises separating two populations of microbial cells, where a first population of separating two populations of microbial cells, where a first population microbial cells populations; amplifying the extracted RNA from both microbial cell populations; amplifying the extracted RNA from both copulations by preparing a collection of at least thirty-two different arbitrary primers, where each primer comprises a common and a variable region; individually contacting each primer of with a sample of extracted RNA from the two populations under conditions where two sets of amplification products are produced; purifying the two sets of amplification products are produced; purifying the two sets of amplification products are produced; purifying the two sets of in the first population which differ from products generated from the second population as differentially expressed genes; and optionally cover previous methods is that previous methods of differential display to chone genes using thirty-two or thirty primers have isolated four and one genes, respectively. The new method using a greater number of primers has

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the environment by an enzymatic degradative process. The present sequence represents a transcription factor encoded by picric acid degradation gene cluster ORFI. (Updated on 29-AUG-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Picric acid degradation; 2,4,6-trinitrophenol; explosive manufacturing; aniline; colour fast dye; pharmaceutical; steel etching; environmental toxicant; enzymatic degradative process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding an F420/NADPH oxidoreductase isolated from Rhodococcus erythropolis HL PM-1 is associated with picric acid degradation and is useful to create recombinant organisms that degrade.
                                                                                       Gaps
                                                                                       ;
                       Length 532;
                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodococcus erythropolis HL PM-1 transcription factor.
                          DB 5; Lei
. 2.7e+02;
                          30.0%; Score 6; DB 5
100.0%; Pred. No. 2.7
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodococcus erythropolis; strain HL-PM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531. .532
/note= "Encoded by GAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 AAU97138 standard; protein; 532 AA.
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Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor.
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The invention relates to a reliable and rapid method to identify differentially expressed genes in microbes. The method relies on the use differentially expressed genes in microbes. The method rise cof a large number of arbitrarily primed PCR reactions. The method is useful for identifying differentially expressed genes in microbes, and for distinguishing genetic differences between two populations of cells which differ in genotype. This method is useful for identifying the DNA sequences of genes involved in the degradation of the picric acid from Rhodococcus expthropolis strain HL PM-1, and genes involved in cyclohexanol degradation from a consortium of organisms, or to detect of a reample of the inhibitory effects of various treatments such as chemicals, environmental pollutants, heavy metals, changes in the emperature, changes in pH, agents producing oxidative damage, agents producing DNA damage, anaerobiosis, pathogenesis, and changes in nitrate availability on mRNA levels. The present sequence is a transcription factor encoded by Rhodococcus erythropolis strain HL PM-1 picric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying differentially expressed genes, by amplifying total RNA of first microbial cell population that is contacted with stimulating agent and of a second population using arbitrary primers, and comparing them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                          Picric acid degradation gene; cyclohexanol degradation; heavy metal; inhibitory effect; chemical; environmental pollutant; anaerobiosis; oxidative damage; pathogenesis; transcription factor.
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Pred. No. 2.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                            Rhodococcus erythropolis HL-PM1 transcription factor.
                                                                                                                                                                                                                                                                                                                                                 Ney
Misc-difference 531. .532
/note= "Encoded by GAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Col 39-42; 51pp; English.
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                       AAE16741 standard; protein; 532 AA.
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                            /label= Glu, Gln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0152542P
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                      Rhodococcus erythropolis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           degradation gene ORF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-121127/16.
SLWALG 337
                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 532
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD27241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rouviere PE;
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                                                                                                                                                           09-APR-2002
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                                                                                                                        AAE16741;
 332
                                                     RESULT 37
                                                                          4AE1674
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6; Conservative

Matches

Query Match Best Local Similarity

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Gaps

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30.0%; Score 6; DB 5; Length 532; 100.0%; Pred. No. 2.7e+02; cive 0; Mismatches 0; Indels

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AAE14907 standard; protein; 548 AA.
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                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                      99WO-US014880
                                                                                                                                                                                                                                                           Glucksmann MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human OCT-5 (57145) protein.
                                                                                                           production"
                          *28. .447
/label= Tr:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                             448.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                      N-PSDB; AAZ49686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 548 AA;
                                                                                                                                                                 WO200000633-A1
                                                                                                                                                                                                                                                            Goodearl AJ,
                                                                                                                                                                                                      29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "shows homology to a consensus sequence for sugar and other transporter molecules derived from a hidden Markov model"
                                                                                                                   Human, organic cation transporter-like protein, OCTIp, transporter, transmembrane; nootropic; neuroprotective; neuroleptic; anticonvulsant; antiparkinsonian, antidepressant; cellular process; cell proliferation; screen, treatment; prevention, diagnosis; neurodegenerative disorder; Alzheimer; Parkinson's; Huntington; ALS; amyotrophic lateral sclerosis; CNS disorder; central nervous system; schizophrenia; depression;
                                                                                                                                                                                                                                                                                                                                                                                         76. .181
|Tabel= Extracellular domain
|tote= "Hydrophilic region useful for antibody
|production"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133. .238
|Jabel= Extracellular_domain
|note= "Hydrophilic region useful for antibody
                                                                                                                                                                                                                                                                                                                /note= "Hydrophilic region useful for antibody
production"
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                                                                                                                                                                         behavioural; sleep disorder; Alzheimer's; eating disorder.
                                                                                                 Human organic cation transporter-like protein (OCTlp).
                                                                                                                                                                                                                                                                                                       label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                   .22. .140
'label= Transmembrane_domain
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label= Extracellular_domain
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/label= Transmembrane_domain
422. .427
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label= Transmembrane_domain
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label= Transmembrane_domain
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                                                                                                                                                                                                                      1. .85
/label= Cytoplasmic_domain
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label= Cytoplasmic_domain
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label= Cytoplasmic_domain
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                                                                                                                                                                                                             Location/Qualifiers
                                            AAY44633 standard; protein; 548 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roduction"
                                                                                                                                                                                                                                                                                                                                                  /label= Cv+
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roduction'
                                                                                (first entry)
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                                                                                                                                                                                                                                         . 524
332 SLWALG 337
                                                                                                                                                                                            Homo sapiens
                                                                                07-APR-2000
                                                             AAY44633;
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                                  AAY44633
                          RESULT
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The present sequence is a human OCTIP (organic cation transporter-like protein), a member of the superfamily of sugar and other transporter molecules that have 12 transmembrane domains. The sequence is derived from a human foetal brain cDNA library. The protein is highly expressed in brain tissue and has nootropic, neuroprotective, neuroleptic, anticonvulsant, antiParkinsonian, antidepressant activities. The present sequence is used to regulate a variety of cellular processes e.g. cell proliferation, differentiation and survival, screen octip modulators and detect mutation in OCTIP gene. OCTIP modulators can be used to treat or prevent chronic neurodegenerative disorders (e.g. Alzheimer's, Parkinson's, Huntington's and ALS), CNS disorders (e.g. schizophrenia, panic, depression), behavioural, sleep and eating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding human organic cation transporter-like protein, used for prevention, treatment and diagnosis of e.g. neurological, behavioral or sleep disorders.
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                                                                                                                                                                                                                                                                                                           180. - 486
| Aabel= Extracellular domain
| Inote= "Hydrophilic region useful for antibody
/label= Extracellular domain
/note= "Hydrophilic region useful for antibody
production"
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                                                                                                                                          Transmembrane domain
                                                                                                                                                                                                                                             58. .479 __ _ __domain
|label= Transmembrane_domain
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/label= Transmembrane_domain
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                                                                                                                                                                        148. 457
/label= Cytoplasmic_domain
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/label= Cytoplasmic_domain
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03-DEC-2002; 2002US-00308163.

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                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method of treating a subject having a activity or nucleic acid expression. The method involves administering a modulator of 577 (also known as sodium dependent proline transporter), 20739 (also known as P21-activated kinase 3 (PAK-3)) or 5745 (also known as OCT-5). The 577, 20739 or 57045 modulator is useful for treating pain disorders like inflammatory pain, chronic pain, neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache pain and tissue pain. The invention also describes methods for diagnosis and prognesis of various cardiovascular disorders, and for identification of subjects exhibiting a predisposition to such conditions. The present sequence is human 57145 protein
                                                                                                                                                                                                                                                                                                                             Treating a subject having a pain disorder characterized by aberrant 577, 20739 or 57145 polypeptide activity or nucleic acid expression, e.g. cancer pain or inflammatory pain, comprises administering a 577, 20739 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rat, levetiracetam, epilepsy; epileptogenesis, seizure disorder; convulsion; depression; anxiety; cerebral ischaemia; myotonia; stroke; Tourette's syndrome; neonatal cerebral haemorrhage; Parkinson's disease; Alzheimer's disease; dementia; synaptic vesicle protein 2; SVOP.
Pain disorder; inflammatory pain; chronic pain; neuropathic pain; causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain; cardiovascular disorder; analgesic; human; 57145; OCT-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 6; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat synaptic vesicle protein 2, SVOP.
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                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 83-84; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Scc_
100.0%; Pred
0; N
                                                                                                                                                         06-NOV-2002; 2002WO-US035562,
                                                                                                                                                                                         06-NOV-2001; 2001US-0333073P.
                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                   WPI; 2003-441438/41.
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                                                                                                                                                                                                                                                                                                   N-PSDB; AAD36883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 548 AA;
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                                                                                                                                                                                                                                                                                                                                                                              57145 modulator.
                                                                                             WO2003039342-A2
                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-2004
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                                                                                                                            15-MAY-2003,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; levetiracetam; epilepsy; epileptogenesis; seizure disorder;
convulsion; depression; anxiety; cerebral ischaemia; myotonia; stroke;
Tourette's syndrome; neonatal cerebral haemorrhage; Parkinson's disease;
Alzheimer's disease; dementia; synaptic vesicle protein 2; SVOP.
                                                                                                                                                                        Identifying binding partner for synaptic vesicle protein 2 (SV2) for treating epilepsy, Parkinson's disease, Alzheimer's disease, involves determining binding partner which modulates binding of levetiracetam or its analog to SV2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.0%; Score 6; DB 8; Length 548; 100.0%; Pred. No. 2.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of the rat synaptic vesicle protein 2, SVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human synaptic vesicle protein 2, SVOP, DNA.
                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 16; 63pp; English.
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                               03-DEC-2002; 2002US-00308163
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                                                                                                                            WPI; 2004-467256/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LGWRWL 13
                                                                                             Nocka K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADO77826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 548 AA;
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                                                                                                                                             N-PSDB; ADO77834
                                                             (UNIO ) UCB SA.
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                                                                                             Lynch B,
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Matches
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ID ADO7
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